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SEQUENCE LISTING

<110> Garvan Institute of Medical Research
Clancy, Jennifer
O'Brien, Phillipa
Saunders, Darren
Henderson, Michelle
Watts, Colin
Sutherland, Robert
Henshall, Susan

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Ser	Leu	Cys	Cys	Cys	Thr	Glu	Cys	Ala	Arg	Val	Cys	His	Lys	Gly
1205					1210						1215			
His	Asp	Cys	Lys	Leu	Lys	Arg	Thr	Ser	Pro	Thr	Ala	Tyr	Cys	Asp
1220					1225						1230			
Cys	Trp	Glu	Lys	Cys	Lys	Cys	Lys	Thr	Leu	Ile	Ala	Gly	Gln	Lys
1235					1240						1245			
Ser	Ala	Arg	Leu	Asp	Leu	Leu	Tyr	Arg	Leu	Leu	Thr	Ala	Thr	Asn
1250					1255						1260			
Leu	Val	Thr	Leu	Pro	Asn	Ser	Arg	Gly	Glu	His	Leu	Leu	Leu	Phe
1265					1270						1275			
Leu	Val	Gln	Thr	Val	Ala	Arg	Gln	Thr	Val	Glu	His	Cys	Gln	Tyr
1280					1285						1290			
Arg	Pro	Pro	Arg	Ile	Arg	Glu	Asp	Arg	Asn	Arg	Lys	Thr	Ala	Ser
1295					1300						1305			
Pro	Glu	Asp	Ser	Asp	Met	Pro	Asp	His	Asp	Leu	Glu	Pro	Pro	Arg
1310					1315						1320			
Phe	Ala	Gln	Leu	Ala	Leu	Glu	Arg	Val	Leu	Gln	Asp	Trp	Asn	Ala
1325					1330						1335			
Leu	Lys	Ser	Met	Ile	Met	Phe	Gly	Ser	Gln	Glu	Asn	Lys	Asp	Pro
1340					1345						1350			
Leu	Ser	Ala	Ser	Ser	Arg	Ile	Gly	His	Leu	Leu	Pro	Glu	Glu	Gln
1355					1360						1365			
Val	Tyr	Leu	Asn	Gln	Gln	Ser	Gly	Thr	Ile	Arg	Leu	Asp	Cys	Phe
1370					1375						1380			
Thr	His	Cys	Leu	Ile	Val	Lys	Cys	Thr	Ala	Asp	Ile	Leu	Leu	Leu
1385					1390						1395			

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Asp Thr	Leu Leu Gly Thr	Leu	Val Lys Glu Leu Gln	Asn Lys Tyr
1400		1405		1410
Thr Pro	Gly Arg Arg Glu	Glu	Ala Ile Ala Val Thr	Met Arg Phe
1415		1420		1425
Leu Arg	Ser Val Ala Arg	Val	Phe Val Ile Leu Ser	Val Glu Met
1430		1435		1440
Ala Ser	Ser Lys Lys Lys	Asn	Asn Phe Ile Pro Gln	Pro Ile Gly
1445		1450		1455
Lys Cys	Lys Arg Val Phe	Gln	Ala Leu Leu Pro Tyr	Ala Val Glu
1460		1465		1470
Glu Leu	Cys Asn Val Ala	Glu	Ser Leu Ile Val Pro	Val Arg Met
1475		1480		1485
Gly Ile	Ala Arg Pro Thr	Ala	Pro Phe Thr Leu Ala	Ser Thr Ser
1490		1495		1500
Ile Asp	Ala Met Gln Gly	Ser	Glu Glu Leu Phe Ser	Val Glu Pro
1505		1510		1515
Leu Pro	Pro Arg Pro Ser	Ser	Asp Gln Ser Ser Ser	Ser Ser Gln
1520		1525		1530
Ser Gln	Ser Ser Tyr Ile	Ile	Arg Asn Pro Gln Gln	Arg Arg Ile
1535		1540		1545
Ser Gln	Ser Gln Pro Val	Arg	Gly Arg Asp Glu Glu	Gln Asp Asp
1550		1555		1560
Ile Val	Ser Ala Asp Val	Glu	Glu Val Glu Val Val	Glu Gly Val
1565		1570		1575
Ala Gly	Glu Glu Asp His	His	Asp Glu Gln Glu Glu	His Gly Glu
1580		1585		1590
Glu Asn	Ala Glu Ala Glu	Gly	Gln His Asp Glu His	Asp Glu Asp
1595		1600		1605
Gly Ser	Asp Met Glu Leu	Asp	Leu Leu Ala Ala Ala	Glu Thr Glu
1610		1615		1620

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Ser Asp 1625 Ser Glu Ser Asn 1630 His 1630 Ser Asn Gln Asp Asn 1635 Ala Ser Gly
 Arg Arg 1640 Ser Val Val Thr Ala 1645 Ala Thr Ala Gly Ser 1650 Glu Ala Gly
 Ala Ser 1655 Ser Val Pro Ala Phe 1660 Phe Ser Glu Asp Asp 1665 Ser Gln Ser
 Asn Asp 1670 Ser Ser Asp Ser Asp 1675 Ser Ser Ser Ser Gln 1680 Ser Asp Asp
 Ile Glu 1685 Gln Glu Thr Phe Met 1690 Leu Asp Glu Pro Leu 1695 Glu Arg Thr
 Thr Asn 1700 Ser Ser His Ala Asn 1705 Gly Ala Ala Gln Ala 1710 Pro Arg Ser
 Met Gln 1715 Trp Ala Val Arg Asn 1720 Thr Gln His Gln Arg 1725 Ala Ala Ser
 Thr Ala 1730 Pro Ser Ser Thr Ser 1735 Thr Pro Ala Ala Ser 1740 Ser Ala Gly
 Leu Ile 1745 Tyr Ile Asp Pro Ser 1750 Asn Leu Arg Arg Ser 1755 Gly Thr Ile
 Ser Thr 1760 Ser Ala Ala Ala Ala 1765 Ala Ala Ala Leu Glu 1770 Ala Ser Asn
 Ala Ser 1775 Ser Tyr Leu Thr Ser 1780 Ala Ser Ser Leu Ala 1785 Arg Ala Tyr
 Ser Ile 1790 Val Ile Arg Gln Ile 1795 Ser Asp Leu Met Gly 1800 Leu Ile Pro
 Lys Tyr 1805 Asn His Leu Val Tyr 1810 Ser Gln Ile Pro Ala 1815 Ala Val Lys
 Leu Thr 1820 Tyr Gln Asp Ala Val 1825 Asn Leu Gln Asn Tyr 1830 Val Glu Glu
 Lys Leu 1835 Ile Pro Thr Trp Asn 1840 Trp Met Val Ser Ile 1845 Met Asp Ser

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Thr Glu Ala Gln Leu Arg Tyr Gly Ser Ala Leu Ala Ser Ala Gly
 1850 1855 1860

Asp Pro Gly His Pro Asn His Pro Leu His Ala Ser Gln Asn Ser
 1865 1870 1875

Ala Arg Arg Glu Arg Met Thr Ala Arg Glu Glu Ala Ser Leu Arg
 1880 1885 1890

Thr Leu Glu Gly Arg Arg Arg Ala Thr Leu Leu Ser Ala Arg Gln
 1895 1900 1905

Gly Met Met Ser Ala Arg Gly Asp Phe Leu Asn Tyr Ala Leu Ser
 1910 1915 1920

Leu Met Arg Ser His Asn Asp Glu His Ser Asp Val Leu Pro Val
 1925 1930 1935

Leu Asp Val Cys Ser Leu Lys His Val Ala Tyr Val Phe Gln Ala
 1940 1945 1950

Leu Ile Tyr Trp Ile Lys Ala Met Asn Gln Gln Thr Thr Leu Asp
 1955 1960 1965

Thr Pro Gln Leu Glu Arg Lys Arg Thr Arg Glu Leu Leu Glu Leu
 1970 1975 1980

Gly Ile Asp Asn Glu Asp Ser Glu His Glu Asn Asp Asp Asp Thr
 1985 1990 1995

Asn Gln Ser Ala Thr Leu Asn Asp Lys Asp Asp Asp Ser Leu Pro
 2000 2005 2010

Ala Glu Thr Gly Gln Asn His Pro Phe Phe Arg Arg Ser Asp Ser
 2015 2020 2025

Met Thr Phe Leu Gly Cys Ile Pro Pro Asn Pro Phe Glu Val Pro
 2030 2035 2040

Leu Ala Glu Ala Ile Pro Leu Ala Asp Gln Pro His Leu Leu Gln
 2045 2050 2055

Pro Asn Ala Arg Lys Glu Asp Leu Phe Gly Arg Pro Ser Gln Gly
 2060 2065 2070

Leu Tyr Ser Ser Ser Ala Ser Ser Gly Lys Cys Leu Met Glu Val

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2075					2080					2085				
Thr	Val	Asp	Arg	Asn	Cys	Leu	Glu	Val	Leu	Pro	Thr	Lys	Met	Ser
	2090					2095					2100			
Tyr	Ala	Ala	Asn	Leu	Lys	Asn	Val	Met	Asn	Met	Gln	Asn	Arg	Gln
	2105					2110					2115			
Lys	Lys	Glu	Gly	Glu	Glu	Gln	Pro	Val	Leu	Pro	Glu	Glu	Thr	Glu
	2120					2125					2130			
Ser	Ser	Lys	Pro	Gly	Pro	Ser	Ala	His	Asp	Leu	Ala	Ala	Gln	Leu
	2135					2140					2145			
Lys	Ser	Ser	Leu	Leu	Ala	Glu	Ile	Gly	Leu	Thr	Glu	Ser	Glu	Gly
	2150					2155					2160			
Pro	Pro	Leu	Thr	Ser	Phe	Arg	Pro	Gln	Cys	Ser	Phe	Met	Gly	Met
	2165					2170					2175			
Val	Ile	Ser	His	Asp	Met	Leu	Leu	Gly	Arg	Trp	Arg	Leu	Ser	Leu
	2180					2185					2190			
Glu	Leu	Phe	Gly	Arg	Val	Phe	Met	Glu	Asp	Val	Gly	Ala	Glu	Pro
	2195					2200					2205			
Gly	Ser	Ile	Leu	Thr	Glu	Leu	Gly	Gly	Phe	Glu	Val	Lys	Glu	Ser
	2210					2215					2220			
Lys	Phe	Arg	Arg	Glu	Met	Glu	Lys	Leu	Arg	Asn	Gln	Gln	Ser	Arg
	2225					2230					2235			
Asp	Leu	Ser	Leu	Glu	Val	Asp	Arg	Asp	Arg	Asp	Leu	Leu	Ile	Gln
	2240					2245					2250			
Gln	Thr	Met	Arg	Gln	Leu	Asn	Asn	His	Phe	Gly	Arg	Arg	Cys	Ala
	2255					2260					2265			
Thr	Thr	Pro	Met	Ala	Val	His	Arg	Val	Lys	Val	Thr	Phe	Lys	Asp
	2270					2275					2280			
Glu	Pro	Gly	Glu	Gly	Ser	Gly	Val	Ala	Arg	Ser	Phe	Tyr	Thr	Ala
	2285					2290					2295			
Ile	Ala	Gln	Ala	Phe	Leu	Ser	Asn	Glu	Lys	Leu	Pro	Asn	Leu	Glu
	2300					2305					2310			

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Cys Ile Gln Asn Ala Asn Lys Gly Thr His Thr Ser Leu Met Gln
 2315 2320 2325
 Arg Leu Arg Asn Arg Gly Glu Arg Asp Arg Glu Arg Glu Arg Glu
 2330 2335 2340
 Arg Glu Met Arg Arg Ser Ser Gly Leu Arg Ala Gly Ser Arg Arg
 2345 2350 2355
 Asp Arg Asp Arg Asp Phe Arg Arg Gln Leu Ser Ile Asp Thr Arg
 2360 2365 2370
 Pro Phe Arg Pro Ala Ser Glu Gly Asn Pro Ser Asp Asp Pro Glu
 2375 2380 2385
 Pro Leu Pro Ala His Arg Gln Ala Leu Gly Glu Arg Leu Tyr Pro
 2390 2395 2400
 Arg Val Gln Ala Met Gln Pro Ala Phe Ala Ser Lys Ile Thr Gly
 2405 2410 2415
 Met Leu Leu Glu Leu Ser Pro Ala Gln Leu Leu Leu Leu Leu Ala
 2420 2425 2430
 Ser Glu Asp Ser Leu Arg Ala Arg Val Asp Glu Ala Met Glu Leu
 2435 2440 2445
 Ile Ile Ala His Gly Arg Glu Asn Gly Ala Asp Ser Ile Leu Asp
 2450 2455 2460
 Leu Gly Leu Val Asp Ser Ser Glu Lys Val Gln Gln Glu Asn Arg
 2465 2470 2475
 Lys Arg His Gly Ser Ser Arg Ser Val Val Asp Met Asp Leu Asp
 2480 2485 2490
 Asp Thr Asp Asp Gly Asp Asp Asn Ala Pro Leu Phe Tyr Gln Pro
 2495 2500 2505
 Gly Lys Arg Gly Phe Tyr Thr Pro Arg Pro Gly Lys Asn Thr Glu
 2510 2515 2520
 Ala Arg Leu Asn Cys Phe Arg Asn Ile Gly Arg Ile Leu Gly Leu
 2525 2530 2535

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Cys Leu Leu Gln Asn Glu Leu Cys Pro Ile Thr Leu Asn Arg His
 2540 2545 2550
 Val Ile Lys Val Leu Leu Gly Arg Lys Val Asn Trp His Asp Phe
 2555 2560 2565
 Ala Phe Phe Asp Pro Val Met Tyr Glu Ser Leu Arg Gln Leu Ile
 2570 2575 2580
 Leu Ala Ser Gln Ser Ser Asp Ala Asp Ala Val Phe Ser Ala Met
 2585 2590 2595
 Asp Leu Ala Phe Ala Ile Asp Leu Cys Lys Glu Glu Gly Gly Gly
 2600 2605 2610
 Gln Val Glu Leu Ile Pro Asn Gly Val Asn Ile Pro Val Thr Pro
 2615 2620 2625
 Gln Asn Val Tyr Glu Tyr Val Arg Lys Tyr Ala Glu His Arg Met
 2630 2635 2640
 Leu Val Val Ala Glu Gln Pro Leu His Ala Met Arg Lys Gly Leu
 2645 2650 2655
 Leu Asp Val Leu Pro Lys Asn Ser Leu Glu Asp Leu Thr Ala Glu
 2660 2665 2670
 Asp Phe Arg Leu Leu Val Asn Gly Cys Gly Glu Val Asn Val Gln
 2675 2680 2685
 Met Leu Ile Ser Phe Thr Ser Phe Asn Asp Glu Ser Gly Glu Asn
 2690 2695 2700
 Ala Glu Lys Leu Leu Gln Phe Lys Arg Trp Phe Trp Ser Ile Val
 2705 2710 2715
 Glu Lys Met Ser Met Thr Glu Arg Gln Asp Leu Val Tyr Phe Trp
 2720 2725 2730
 Thr Ser Ser Pro Ser Leu Pro Ala Ser Glu Glu Gly Phe Gln Pro
 2735 2740 2745
 Met Pro Ser Ile Thr Ile Arg Pro Pro Asp Asp Gln His Leu Pro
 2750 2755 2760

Thr Ala Asn Thr Cys Ile Ser Arg Leu Tyr Val Pro Leu Tyr Ser
2765 2770 2775

Ser Lys Gln Ile Leu Lys Gln Lys Leu Leu Leu Ala Ile Lys Thr
2780 2785 2790

Lys Asn Phe Gly Phe Val
2795

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<223>
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- 19 -

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ggg tct ggg ctt ttg ggc agt cag ccc cag cca gtt att cca gca tct Gly Ser Gly Leu Leu Gly Ser Gln Pro Gln Pro Val Ile Pro Ala Ser 170 175 180			582
gtc att cca gag gag ctg att tca cag gcc caa gtt gtt tta caa ggc Val Ile Pro Glu Glu Leu Ile Ser Gln Ala Gln Val Val Leu Gln Gly 185 190 195			630
aaa tcc aga agt gtc att att cga gaa ctt cag aga aca aat ctt gat Lys Ser Arg Ser Val Ile Ile Arg Glu Leu Gln Arg Thr Asn Leu Asp 200 205 210 215			678
gtg aac ctt gct gta aat aat tta ctt agc cgg gat gat gaa gat gga Val Asn Leu Ala Val Asn Asn Leu Leu Ser Arg Asp Asp Glu Asp Gly 220 225 230			726
gat gat ggg gat gat aca gcc agc gaa tct tat ttg cct gga gag gat Asp Asp Gly Asp Asp Thr Ala Ser Glu Ser Tyr Leu Pro Gly Glu Asp 235 240 245			774
ctt atg tct ctc ctt gat gcc gac att cat tct gcc cac cca agt gtc Leu Met Ser Leu Leu Asp Ala Asp Ile His Ser Ala His Pro Ser Val 250 255 260			822
att att gat gca gat gcc atg ttt tct gaa gac att agc tat ttt ggt Ile Ile Asp Ala Asp Ala Met Phe Ser Glu Asp Ile Ser Tyr Phe Gly 265 270 275			870
tac cct tct ttt cgt cgt tca tca ctt tcc agg cta ggc tca tct cga Tyr Pro Ser Phe Arg Arg Ser Ser Leu Ser Arg Leu Gly Ser Ser Arg 280 285 290 295			918
gag aga gac tct gag ctg ttg cgt gaa cgt gaa tcc gtt tta cgt tta Glu Arg Asp Ser Glu Leu Leu Arg Glu Arg Glu Ser Val Leu Arg Leu 300 305 310			966
cgt gaa cga agg tgg ctt gat gga gcc tca ttt gat aat gaa agg ggt Arg Glu Arg Arg Trp Leu Asp Gly Ala Ser Phe Asp Asn Glu Arg Gly 315 320 325			1014
tct acc agc aag gaa gga gag cca aac ttg gat aag aag aat aca cct Ser Thr Ser Lys Glu Gly Glu Pro Asn Leu Asp Lys Lys Asn Thr Pro 330 335 340			1062
gtt caa agt cca gta tct cta gga gaa gat ttg cag tgg tgg cct gat Val Gln Ser Pro Val Ser Leu Gly Glu Asp Leu Gln Trp Trp Pro Asp 345 350 355			1110
aag gat gga aca aaa ttc atc tgt att ggg gct ctg tat tct gaa ctt Lys Asp Gly Thr Lys Phe Ile Cys Ile Gly Ala Leu Tyr Ser Glu Leu 360 365 370 375			1158
ctg gct gtc agc agt aaa gga gaa ctt tat cag tgg aaa tgg agt gaa Leu Ala Val Ser Ser Lys Gly Glu Leu Tyr Gln Trp Lys Trp Ser Glu 380 385 390			1206

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tct gag cct tac aga aat gcc cag aat cct tca tta cat cat cca cga Ser Glu Pro Tyr Arg Asn Ala Gln Asn Pro Ser Leu His His Pro Arg 395 400 405	1254
gca aca ttt ttg ggg tta acc aat gaa aag ata gtc ctc ctg tct gca Ala Thr Phe Leu Gly Leu Thr Asn Glu Lys Ile Val Leu Leu Ser Ala 410 415 420	1302
aat agc ata aga gca act gta gct aca gaa aat aac aag gtt gct aca Asn Ser Ile Arg Ala Thr Val Ala Thr Glu Asn Asn Lys Val Ala Thr 425 430 435	1350
tgg gtg gat gaa act tta agt tct gtg gct tct aaa tta gag cac act Trp Val Asp Glu Thr Leu Ser Ser Val Ala Ser Lys Leu Glu His Thr 440 445 450 455	1398
gct cag act tac tct gaa ctt caa gga gag cgg ata gtt tct tta cat Ala Gln Thr Tyr Ser Glu Leu Gln Gly Glu Arg Ile Val Ser Leu His 460 465 470	1446
tgc tgt gcc ctt tac acc tgc gct cag ctg gaa aac agt tta tat tgg Cys Cys Ala Leu Tyr Thr Cys Ala Gln Leu Glu Asn Ser Leu Tyr Trp 475 480 485	1494
tgg ggt gta gtt cct ttt agt caa agg aag aaa atg tta gag aaa gct Trp Gly Val Val Pro Phe Ser Gln Arg Lys Lys Met Leu Glu Lys Ala 490 495 500	1542
aga gca aaa aat aaa aag cct aaa tcc agt gct ggt att tct tca atg Arg Ala Lys Asn Lys Lys Pro Lys Ser Ser Ala Gly Ile Ser Ser Met 505 510 515	1590
ccg aac atc act gtt ggt acc cag gta tgc ttg aga aat aat cct ctt Pro Asn Ile Thr Val Gly Thr Gln Val Cys Leu Arg Asn Asn Pro Leu 520 525 530 535	1638
tat cat gct gga gca gtt gca ttt tca att agt gct ggg att cct aaa Tyr His Ala Gly Ala Val Ala Phe Ser Ile Ser Ala Gly Ile Pro Lys 540 545 550	1686
gtt ggt gtc tta atg gag tca gtt tgg aat atg aat gac agc tgt aga Val Gly Val Leu Met Glu Ser Val Trp Asn Met Asn Asp Ser Cys Arg 555 560 565	1734
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aaa act act gaa gct aag cct gaa agt aag cag gag cca gtg aaa aca Lys Thr Thr Glu Ala Lys Pro Glu Ser Lys Gln Glu Pro Val Lys Thr 585 590 595	1830
gaa atg ggt cct cca cca tct cca gca tcc acg tgt agt gat gca tcc Glu Met Gly Pro Pro Ser Pro Ala Ser Thr Cys Ser Asp Ala Ser 600 605 610 615	1878
tca att gcc agc agt gca tca atg cca tac aaa cga cga cgg tca acc Ser Ile Ala Ser Ser Ala Ser Met Pro Tyr Lys Arg Arg Arg Ser Thr 620 625 630	1926

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cct gca cca aaa gaa gag gaa aag gtg aat gaa gag cag tgg tct ctt Pro Ala Pro Lys Glu Glu Glu Lys Val Asn Glu Glu Gln Trp Ser Leu 635 640 645	1974
cgg gaa gtg gtt ttt gtg gaa gat gtc aag aat gtt cct gtt ggc aag Arg Glu Val Val Phe Val Glu Asp Val Lys Asn Val Pro Val Gly Lys 650 655 660	2022
gtg cta aaa gta gat ggt gcc tat gtt gct gta aaa ttt cca gga acc Val Leu Lys Val Asp Gly Ala Tyr Val Ala Val Lys Phe Pro Gly Thr 665 670 675	2070
tcc agt aat act aac tgt cag aac agc tct ggt cca gat gct gac cct Ser Ser Asn Thr Asn Cys Gln Asn Ser Ser Gly Pro Asp Ala Asp Pro 680 685 690 695	2118
tct tct ctc ctg cag gat tgt agg tta ctt aga att gat gaa ttg cag Ser Ser Leu Leu Gln Asp Cys Arg Leu Leu Arg Ile Asp Glu Leu Gln 700 705 710	2166
gtt gtc aaa act ggt gga aca ccg aag gtt ccc gac tgt ttc caa agg Val Val Lys Thr Gly Gly Thr Pro Lys Val Pro Asp Cys Phe Gln Arg 715 720 725	2214
act cct aaa aag ctt tgt ata cct gaa aaa aca gaa ata tta gca gtg Thr Pro Lys Lys Leu Cys Ile Pro Glu Lys Thr Glu Ile Leu Ala Val 730 735 740	2262
aat gta gat tcc aaa ggt gtt cat gct gtt ctg aag act gga aat tgg Asn Val Asp Ser Lys Gly Val His Ala Val Leu Lys Thr Gly Asn Trp 745 750 755	2310
gtg cga tac tgt atc ttt gat ctt gct aca gga aaa gca gaa cag gaa Val Arg Tyr Cys Ile Phe Asp Leu Ala Thr Gly Lys Ala Glu Gln Glu 760 765 770 775	2358
aat aat ttt cct aca agc agc att gct ttc ctt ggt cag aat gag agg Asn Asn Phe Pro Thr Ser Ser Ile Ala Phe Leu Gly Gln Asn Glu Arg 780 785 790	2406
aat gta gcc att ttc act gct gga cag gaa tct ccc att att ctt cga Asn Val Ala Ile Phe Thr Ala Gly Gln Glu Ser Pro Ile Ile Leu Arg 795 800 805	2454
gat gga aat ggt acc atc tac cca atg gcc aaa gat tgc atg gga gga Asp Gly Asn Gly Thr Ile Tyr Pro Met Ala Lys Asp Cys Met Gly Gly 810 815 820	2502
ata agg gat ccc gat tgg ctg gat ctt cca cct att agt agt ctt gga Ile Arg Asp Pro Asp Trp Leu Asp Leu Pro Pro Ile Ser Ser Leu Gly 825 830 835	2550
atg ggt gtg cat tct tta ata aat ctt cct gcc aat tca aca atc aaa Met Gly Val His Ser Leu Ile Asn Leu Pro Ala Asn Ser Thr Ile Lys 840 845 850 855	2598
aag aaa gct gct gtt atc atc atg gct gta gag aaa caa acc tta atg Lys Lys Ala Ala Val Ile Ile Met Ala Val Glu Lys Gln Thr Leu Met 860 865 870	2646
caa cac att ctg cgc tgt gac tat gag gcc tgt cga caa tat cta atg	2694

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Gln His Ile Leu Arg Cys Asp Tyr Glu Ala Cys Arg Gln Tyr Leu Met	
875 880 885	
aat ctt gag caa gcg gtt gtt tta gag cag aat cta cag atg ctg cag	2742
Asn Leu Glu Gln Ala Val Val Leu Glu Gln Asn Leu Gln Met Leu Gln	
890 895 900	
aca ttc atc agc cac aga tgt gat gga aat cga aat att ttg cat gct	2790
Thr Phe Ile Ser His Arg Cys Asp Gly Asn Arg Asn Ile Leu His Ala	
905 910 915	
tgt gta tca gtt tgc ttt cca acc agc aat aaa gaa act aaa gaa gaa	2838
Cys Val Ser Val Cys Phe Pro Thr Ser Asn Lys Glu Thr Lys Glu Glu	
920 925 930 935	
gag gaa gcg gag cgt tct gaa aga aat aca ttt gca gaa agg ctt tct	2886
Glu Glu Ala Glu Arg Ser Glu Arg Asn Thr Phe Ala Glu Arg Leu Ser	
940 945 950	
gct gtt gag gcc att gca aat gca ata tca gtt gtt tca agt aat ggc	2934
Ala Val Glu Ala Ile Ala Asn Ala Ile Ser Val Val Ser Ser Asn Gly	
955 960 965	
cca ggt aat cgg gct gga tca tca agt agc cga agt ttg aga tta cgg	2982
Pro Gly Asn Arg Ala Gly Ser Ser Ser Ser Arg Ser Leu Arg Leu Arg	
970 975 980	
gaa atg atg aga cgt tcg ttg aga gca gct ggt ttg ggt aga cat gaa	3030
Glu Met Met Arg Arg Ser Leu Arg Ala Ala Gly Leu Gly Arg His Glu	
985 990 995	
gct gga gct tca tcc agt gac cac cag gat cca gtt tca ccc ccc	3075
Ala Gly Ala Ser Ser Ser Asp His Gln Asp Pro Val Ser Pro Pro	
1000 1005 1010	
ata gct ccc cct agt tgg gtt cct gac cct cct gcg atg gat cct	3120
Ile Ala Pro Pro Ser Trp Val Pro Asp Pro Pro Ala Met Asp Pro	
1015 1020 1025	
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Asp Gly Asp Ile Asp Phe Ile Leu Ala Pro Ala Val Gly Ser Leu	
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acc aca gca gca acc ggt act ggt caa gga cca agc acc tcc act	3210
Thr Thr Ala Ala Thr Gly Thr Gly Gln Gly Pro Ser Thr Ser Thr	
1045 1050 1055	
att cca ggt cct tcc aca gag cca tct gta gta gaa tcc aag gat	3255
Ile Pro Gly Pro Ser Thr Glu Pro Ser Val Val Glu Ser Lys Asp	
1060 1065 1070	
cga aag gcg aat gct cat ttt ata ttg aaa ttg tta tgt gac agt	3300
Arg Lys Ala Asn Ala His Phe Ile Leu Lys Leu Leu Cys Asp Ser	
1075 1080 1085	
gtg gtt ctc cag ccc tat cta cga gaa ctt ctt tct gcc aag gat	3345
Val Val Leu Gln Pro Tyr Leu Arg Glu Leu Leu Ser Ala Lys Asp	
1090 1095 1100	
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Ala Arg Gly Met Thr Pro Phe Met Ser Ala Val Ser Gly Arg Ala	

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1105		1110		1115	
tat	cct gct gca att acc	atc tta gaa act	gct	cag aaa att gca	3435
Tyr	Pro Ala Ala Ile Thr	Ile Leu Glu Thr	Ala	Gln Lys Ile Ala	
1120		1125		1130	
aaa	gct gaa ata tcc tca	agt gaa aaa gag	gaa	gat gta ttc atg	3480
Lys	Ala Glu Ile Ser Ser	Ser Glu Lys Glu	Glu	Asp Val Phe Met	
1135		1140		1145	
gga	atg gtt tgc cca tca	ggt acc aac cct	gat	gac tct cct tta	3525
Gly	Met Val Cys Pro Ser	Gly Thr Asn Pro	Asp	Asp Ser Pro Leu	
1150		1155		1160	
tat	gtt tta tgt tgt aat	gac act tgc agt	ttt	aca tgg act gga	3570
Tyr	Val Leu Cys Cys Asn	Asp Thr Cys Ser	Phe	Thr Trp Thr Gly	
1165		1170		1175	
gca	gag cac att aac cag	gat att ttt gag	tgt	cga act tgt ggc	3615
Ala	Glu His Ile Asn Gln	Asp Ile Phe Glu	Cys	Arg Thr Cys Gly	
1180		1185		1190	
ttg	ctg gag tca ctg tgt	tgt tgt acg gaa	tgt	gca agg gtt tgt	3660
Leu	Leu Glu Ser Leu Cys	Cys Cys Thr Glu	Cys	Ala Arg Val Cys	
1195		1200		1205	
cat	aaa ggt cat gat tgc	aaa ctc aaa cgg	aca	tca cca aca gcc	3705
His	Lys Gly His Asp Cys	Lys Leu Lys Arg	Thr	Ser Pro Thr Ala	
1210		1215		1220	
tac	tgt gat tgt tgg gag	aaa tgt aaa tgt	aaa	act ctt att gct	3750
Tyr	Cys Asp Cys Trp Glu	Lys Cys Lys Cys	Lys	Thr Leu Ile Ala	
1225		1230		1235	
gga	cag aaa tct gct cgt	ctt gat cta ctt	tat	cgc ctg ctc act	3795
Gly	Gln Lys Ser Ala Arg	Leu Asp Leu Leu	Tyr	Arg Leu Leu Thr	
1240		1245		1250	
gct	act aat ctg gtt act	ctg cca aac agc	agg	gga gag cac ctc	3840
Ala	Thr Asn Leu Val Thr	Leu Pro Asn Ser	Arg	Gly Glu His Leu	
1255		1260		1265	
tta	cta ttc tta gta cag	aca gtc gca agg	cag	acg gtg gag cat	3885
Leu	Leu Phe Leu Val Gln	Thr Val Ala Arg	Gln	Thr Val Glu His	
1270		1275		1280	
tgt	caa tac agg cca cct	cga atc agg gaa	gat	cgt aac cga aaa	3930
Cys	Gln Tyr Arg Pro Pro	Arg Ile Arg Glu	Asp	Arg Asn Arg Lys	
1285		1290		1295	
aca	gcc agt cct gaa gat	tca gat atg cca	gat	cat gat tta gag	3975
Thr	Ala Ser Pro Glu Asp	Ser Asp Met Pro	Asp	His Asp Leu Glu	
1300		1305		1310	
cct	cca aga ttt gcc cag	ctt gca ttg gag	cgt	gtt cta cag gac	4020
Pro	Pro Arg Phe Ala Gln	Leu Ala Leu Glu	Arg	Val Leu Gln Asp	
1315		1320		1325	
tgg	aat gcc ttg aaa tct	atg att atg ttt	ggg	tcg cag gag aat	4065
Trp	Asn Ala Leu Lys Ser	Met Ile Met Phe	Gly	Ser Gln Glu Asn	
1330		1335		1340	

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aaa gac cct ctt agt gcc agc agt aga ata ggc cat ctt ttg cca Lys Asp Pro Leu Ser Ala Ser Ser Arg Ile Gly His Leu Leu Pro 1345 1350 1355	4110
gaa gag caa gta tac ctc aat cag caa agt ggc aca att cgg ctg Glu Glu Gln Val Tyr Leu Asn Gln Gln Ser Gly Thr Ile Arg Leu 1360 1365 1370	4155
gac tgt ttc act cat tgc ctt ata gtt aag tgt aca gca gat att Asp Cys Phe Thr His Cys Leu Ile Val Lys Cys Thr Ala Asp Ile 1375 1380 1385	4200
ttg ctt tta gat act cta cta ggt aca cta gtg aaa gaa ctc caa Leu Leu Leu Asp Thr Leu Leu Gly Thr Leu Val Lys Glu Leu Gln 1390 1395 1400	4245
aac aaa tat aca cct gga cgt aga gaa gaa gct att gct gtg aca Asn Lys Tyr Thr Pro Gly Arg Arg Glu Glu Ala Ile Ala Val Thr 1405 1410 1415	4290
atg agg ttt cta cgt tca gtg gca aga gtt ttt gtt att ctg agt Met Arg Phe Leu Arg Ser Val Ala Arg Val Phe Val Ile Leu Ser 1420 1425 1430	4335
gtg gaa atg gct tca tcc aaa aag aaa aac aac ttt att cca cag Val Glu Met Ala Ser Ser Lys Lys Lys Asn Asn Phe Ile Pro Gln 1435 1440 1445	4380
cca att gga aaa tgc aag cgt gta ttc caa gca ttg cta cct tac Pro Ile Gly Lys Cys Lys Arg Val Phe Gln Ala Leu Leu Pro Tyr 1450 1455 1460	4425
gct gtg gaa gaa ttg tgc aac gta gca gag tca ctg att gtt cct Ala Val Glu Glu Leu Cys Asn Val Ala Glu Ser Leu Ile Val Pro 1465 1470 1475	4470
gtc aga atg ggg att gct cgt cca act gca cca ttt acc ctg gct Val Arg Met Gly Ile Ala Arg Pro Thr Ala Pro Phe Thr Leu Ala 1480 1485 1490	4515
agt act agc ata gat gcc atg cag ggc agt gaa gaa tta ttt tca Ser Thr Ser Ile Asp Ala Met Gln Gly Ser Glu Glu Leu Phe Ser 1495 1500 1505	4560
gtg gaa cca cta cca cca cga cca tca tct gat cag tct agc agc Val Glu Pro Leu Pro Pro Arg Pro Ser Ser Asp Gln Ser Ser Ser 1510 1515 1520	4605
tcc agt cag tct cag tca tcc tac atc atc agg aat cca cag cag Ser Ser Gln Ser Gln Ser Ser Tyr Ile Ile Arg Asn Pro Gln Gln 1525 1530 1535	4650
agg cgc atc agc cag tca cag ccc gtt cgg ggc aga gat gaa gaa Arg Arg Ile Ser Gln Ser Gln Pro Val Arg Gly Arg Asp Glu Glu 1540 1545 1550	4695
cag gat gat att gtt tca gca gat gtg gaa gag gtt gag gtg gtg Gln Asp Asp Ile Val Ser Ala Asp Val Glu Glu Val Glu Val Val 1555 1560 1565	4740

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gag Glu 1570	ggt Gly	gtg Val	gct Ala	gga Gly	gaa Glu 1575	gag Glu	gat Asp	cat His	cat His	gat Asp 1580	gaa Glu	cag Gln	gaa Glu	gaa Glu	4785
cac His 1585	ggg Gly	gaa Glu	gaa Glu	aat Asn	gct Ala 1590	gag Glu	gca Ala	gag Glu	gga Gly	caa Gln 1595	cat His	gat Asp	gag Glu	cat His	4830
gat Asp 1600	gaa Glu	gac Asp	ggg Gly	agt Ser	gat Asp 1605	atg Met	gag Glu	ctg Leu	gac Asp	ttg Leu 1610	tta Leu	gca Ala	gca Ala	gct Ala	4875
gaa Glu 1615	aca Thr	gaa Glu	agt Ser	gat Asp	agt Ser 1620	gaa Glu	agt Ser	aac Asn	cac His	agc Ser 1625	aac Asn	caa Gln	gat Asp	aat Asn	4920
gct Ala 1630	agt Ser	ggg Gly	cgc Arg	aga Arg	agc Ser 1635	gtt Val	gtc Val	act Thr	gca Ala	gca Ala 1640	act Thr	gct Ala	ggt Gly	tca Ser	4965
gaa Glu 1645	gca Ala	gga Gly	gca Ala	agc Ser	agt Ser 1650	gtt Val	cct Pro	gcc Ala	ttc Phe	ttt Phe 1655	tct Ser	gaa Glu	gat Asp	gat Asp	5010
tct Ser 1660	caa Gln	tcg Ser	aat Asn	gac Asp	tca Ser 1665	agt Ser	gat Asp	tct Ser	gat Asp	agc Ser 1670	agt Ser	agt Ser	agt Ser	cag Gln	5055
agt Ser 1675	gac Asp	gac Asp	ata Ile	gaa Glu	cag Gln 1680	gag Glu	acc Thr	ttt Phe	atg Met	ctt Leu 1685	gat Asp	gag Glu	cca Pro	tta Leu	5100
gaa Glu 1690	aga Arg	acc Thr	aca Thr	aat Asn	agc Ser 1695	tcc Ser	cat His	gcc Ala	aat Asn	ggg Gly 1700	gct Ala	gcc Ala	caa Gln	gct Ala	5145
ccc Pro 1705	cgt Arg	tca Ser	atg Met	cag Gln	tgg Trp 1710	gct Ala	gtc Val	cgc Arg	aac Asn	acc Thr 1715	cag Gln	cat His	cag Gln	cga Arg	5190
gca Ala 1720	gcc Ala	agt Ser	aca Thr	gcc Ala	cct Pro 1725	tcc Ser	agt Ser	aca Thr	tct Ser	aca Thr 1730	cca Pro	gca Ala	gca Ala	agt Ser	5235
tca Ser 1735	gcg Ala	ggt Gly	ttg Leu	att Ile	tat Tyr 1740	att Ile	gat Asp	cct Pro	tca Ser	aac Asn 1745	tta Leu	cgc Arg	cgg Arg	agt Ser	5280
ggt Gly 1750	acc Thr	atc Ile	agt Ser	aca Thr	agt Ser 1755	gct Ala	gca Ala	gct Ala	gca Ala	gca Ala 1760	gct Ala	gct Ala	ttg Leu	gaa Glu	5325
gct Ala 1765	agc Ser	aac Asn	gcc Ala	agc Ser	agt Ser 1770	tac Tyr	cta Leu	aca Thr	tct Ser	gca Ala 1775	agc Ser	agt Ser	tta Leu	gcc Ala	5370
agg Arg 1780	gct Ala	tac Tyr	agc Ser	att Ile	gtc Val 1785	att Ile	aga Arg	caa Gln	atc Ile	tcg Ser 1790	gac Asp	ttg Leu	atg Met	ggc Gly	5415
ctt	att	cct	aag	tat	aat	cac	cta	gta	tac	tct	cag	att	cca	gca	5460

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Leu 1795	Ile	Pro	Lys	Tyr	Asn 1800	His	Leu	Val	Tyr	Ser 1805	Gln	Ile	Pro	Ala	
gct Ala 1810	gtg Val	aaa Lys	ttg Leu	act Thr	tac Tyr 1815	caa Gln	gat Asp	gca Ala	gta Val	aac Asn 1820	tta Leu	cag Gln	aac Asn	tat Tyr	5505
gta Val 1825	gaa Glu	gaa Glu	aag Lys	ctt Leu	att Ile 1830	ccc Pro	act Thr	tgg Trp	aac Asn	tgg Trp 1835	atg Met	gtc Val	agt Ser	att Ile	5550
atg Met 1840	gat Asp	tct Ser	act Thr	gaa Glu	gct Ala 1845	caa Gln	tta Leu	cgt Arg	tat Tyr	ggt Gly 1850	tct Ser	gca Ala	tta Leu	gca Ala	5595
tct Ser 1855	gct Ala	ggt Gly	gat Asp	cct Pro	gga Gly 1860	cat His	cca Pro	aat Asn	cat His	cct Pro 1865	ctt Leu	cac His	gct Ala	tct Ser	5640
cag Gln 1870	aat Asn	tca Ser	gcg Ala	aga Arg	aga Arg 1875	gag Glu	agg Arg	atg Met	act Thr	gcg Ala 1880	cga Arg	gaa Glu	gaa Glu	gct Ala	5685
agc Ser 1885	tta Leu	cga Arg	aca Thr	ctt Leu	gaa Glu 1890	ggc Gly	aga Arg	cga Arg	cgt Arg	gcc Ala 1895	acc Thr	ttg Leu	ctt Leu	agc Ser	5730
gcc Ala 1900	cgt Arg	caa Gln	gga Gly	atg Met	atg Met 1905	tct Ser	gca Ala	cga Arg	gga Gly	gac Asp 1910	ttc Phe	cta Leu	aat Asn	tat Tyr	5775
gct Ala 1915	ctg Leu	tct Ser	cta Leu	atg Met	cgg Arg 1920	tct Ser	cat His	aat Asn	gat Asp	gag Glu 1925	cat His	tct Ser	gat Asp	gtt Val	5820
ctt Leu 1930	cca Pro	gtt Val	ttg Leu	gat Asp	gtt Val 1935	tgc Cys	tca Ser	ttg Leu	aag Lys	cat His 1940	gtg Val	gca Ala	tat Tyr	gtt Val	5865
ttt Phe 1945	caa Gln	gca Ala	ctt Leu	ata Ile	tac Tyr 1950	tgg Trp	att Ile	aag Lys	gca Ala	atg Met 1955	aat Asn	cag Gln	cag Gln	aca Thr	5910
aca Thr 1960	ttg Leu	gat Asp	aca Thr	cct Pro	caa Gln 1965	cta Leu	gaa Glu	cgc Arg	aaa Lys	agg Arg 1970	acg Thr	cga Arg	gaa Glu	ctc Leu	5955
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gat Asp 1990	gac Asp	acc Thr	aat Asn	caa Gln	agt Ser 1995	gct Ala	act Thr	ttg Leu	aat Asn	gat Asp 2000	aag Lys	gat Asp	gat Asp	gac Asp	6045
tct Ser 2005	ctt Leu	cct Pro	gca Ala	gaa Glu	act Thr 2010	ggc Gly	caa Gln	aac Asn	cat His	cca Pro 2015	ttt Phe	ttc Phe	cga Arg	cgt Arg	6090
tca Ser	gac Asp	tcc Ser	atg Met	aca Thr	ttc Phe	ctt Leu	ggg Gly	tgt Cys	ata Ile	ccc Pro	cca Pro	aat Asn	cca Pro	ttt Phe	6135

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2020	2025					2030										
gaa Glu 2035	gtg Val	cct Pro	ctg Leu	gct Ala	gaa Glu 2040	gcc Ala	atc Ile	ccc Pro	ttg Leu	gct Ala 2045	gat Asp	cag Gln	cca Pro	cat His		6180
ctg Leu 2050	ttg Leu	cag Gln	cca Pro	aat Asn	gct Ala 2055	aga Arg	aag Lys	gag Glu	gat Asp	ctt Leu 2060	ttt Phe	ggc Gly	cgt Arg	cca Pro		6225
agt Ser 2065	cag Gln	ggt Gly	ctt Leu	tat Tyr	tct Ser 2070	tca Ser	tct Ser	gcc Ala	agt Ser	agt Ser 2075	ggg Gly	aaa Lys	tgt Cys	tta Leu		6270
atg Met 2080	gag Glu	gtt Val	aca Thr	gtg Val	gat Asp 2085	aga Arg	aac Asn	tgc Cys	cta Leu	gag Glu 2090	gtt Val	ctt Leu	cca Pro	aca Thr		6315
aaa Lys 2095	atg Met	tct Ser	tat Tyr	gct Ala	gcc Ala 2100	aat Asn	ctg Leu	aaa Lys	aat Asn	gta Val 2105	atg Met	aac Asn	atg Met	caa Gln		6360
aac Asn 2110	cgg Arg	caa Gln	aaa Lys	aaa Lys	gaa Glu 2115	ggg Gly	gaa Glu	gaa Glu	cag Gln	ccc Pro 2120	gtg Val	ctg Leu	cca Pro	gaa Glu		6405
gaa Glu 2125	act Thr	gag Glu	agt Ser	tca Ser	aaa Lys 2130	cca Pro	ggg Gly	cca Pro	tct Ser	gct Ala 2135	cat His	gat Asp	ctt Leu	gct Ala		6450
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agt Ser 2155	gaa Glu	ggg Gly	cca Pro	cct Pro	ctc Leu 2160	aca Thr	tct Ser	ttc Phe	agg Arg	cca Pro 2165	cag Gln	tgt Cys	agc Ser	ttt Phe		6540
atg Met 2170	gga Gly	atg Met	gtt Val	att Ile	tcc Ser 2175	cat His	gat Asp	atg Met	ctg Leu	cta Leu 2180	gga Gly	cgt Arg	tgg Trp	cgc Arg		6585
ctt Leu 2185	tct Ser	tta Leu	gaa Glu	ctg Leu	ttc Phe 2190	ggc Gly	agg Arg	gta Val	ttc Phe	atg Met 2195	gaa Glu	gat Asp	gtt Val	gga Gly		6630
gca Ala 2200	gaa Glu	cct Pro	gga Gly	tca Ser	atc Ile 2205	cta Leu	act Thr	gaa Glu	ttg Leu	ggt Gly 2210	ggt Gly	ttt Phe	gag Glu	gta Val		6675
aaa Lys 2215	gaa Glu	tca Ser	aaa Lys	ttc Phe	cgc Arg 2220	aga Arg	gaa Glu	atg Met	gaa Glu	aaa Lys 2225	ctg Leu	aga Arg	aac Asn	cag Gln		6720
cag Gln 2230	tca Ser	aga Arg	gat Asp	ttg Leu	tca Ser 2235	cta Leu	gag Glu	gtt Val	gat Asp	cgg Arg 2240	gat Asp	cga Arg	gat Asp	ctt Leu		6765
ctc Leu 2245	att Ile	cag Gln	cag Gln	act Thr	atg Met 2250	agg Arg	cag Gln	ctt Leu	aac Asn	aat Asn 2255	cac His	ttt Phe	ggt Gly	cga Arg		6810

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aga	tgt	gct	act	aca	cca	atg	gct	gta	cac	aga	gta	aaa	gtc	aca	6855
Arg	Cys	Ala	Thr	Thr	Pro	Met	Ala	Val	His	Arg	Val	Lys	Val	Thr	
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Phe	Lys	Asp	Glu	Pro	Gly	Glu	Gly	Ser	Gly	Val	Ala	Arg	Ser	Phe	
2275					2280					2285					
tat	aca	gcc	att	gca	caa	gca	ttt	tta	tca	aat	gaa	aaa	ttg	cca	6945
Tyr	Thr	Ala	Ile	Ala	Gln	Ala	Phe	Leu	Ser	Asn	Glu	Lys	Leu	Pro	
2290					2295					2300					
aat	cta	gag	tgt	atc	caa	aat	gcc	aac	aaa	ggc	acc	cac	aca	agt	6990
Asn	Leu	Glu	Cys	Ile	Gln	Asn	Ala	Asn	Lys	Gly	Thr	His	Thr	Ser	
2305					2310					2315					
tta	atg	cag	aga	tta	agg	aac	cga	gga	gag	aga	gac	cgg	gaa	agg	7035
Leu	Met	Gln	Arg	Leu	Arg	Asn	Arg	Gly	Glu	Arg	Asp	Arg	Glu	Arg	
2320					2325					2330					
gag	aga	gaa	agg	gaa	atg	agg	agg	agt	agt	ggt	ttg	cga	gca	ggt	7080
Glu	Arg	Glu	Arg	Glu	Met	Arg	Arg	Ser	Ser	Gly	Leu	Arg	Ala	Gly	
2335					2340					2345					
tct	cgg	agg	gac	cgg	gat	aga	gac	ttt	aga	aga	cag	ctt	tcc	atc	7125
Ser	Arg	Arg	Asp	Arg	Asp	Arg	Asp	Phe	Arg	Arg	Gln	Leu	Ser	Ile	
2350					2355					2360					
gac	act	agg	ccc	ttt	aga	cca	gcc	tct	gaa	ggg	aat	cct	agc	gat	7170
Asp	Thr	Arg	Pro	Phe	Arg	Pro	Ala	Ser	Glu	Gly	Asn	Pro	Ser	Asp	
2365					2370					2375					
gat	cct	gag	cct	ttg	cca	gca	cat	cgg	cag	gca	ctt	gga	gag	agg	7215
Asp	Pro	Glu	Pro	Leu	Pro	Ala	His	Arg	Gln	Ala	Leu	Gly	Glu	Arg	
2380					2385					2390					
ctt	tat	cct	cgt	gta	caa	gca	atg	caa	cca	gca	ttt	gca	agt	aaa	7260
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Ile	Thr	Gly	Met	Leu	Leu	Glu	Leu	Ser	Pro	Ala	Gln	Leu	Leu	Leu	
2410					2415					2420					
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Leu	Leu	Ala	Ser	Glu	Asp	Ser	Leu	Arg	Ala	Arg	Val	Asp	Glu	Ala	
2425					2430					2435					
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Met	Glu	Leu	Ile	Ile	Ala	His	Gly	Arg	Glu	Asn	Gly	Ala	Asp	Ser	
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Ile	Leu	Asp	Leu	Gly	Leu	Val	Asp	Ser	Ser	Glu	Lys	Val	Gln	Gln	
2455					2460					2465					
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Glu	Asn	Arg	Lys	Arg	His	Gly	Ser	Ser	Arg	Ser	Val	Val	Asp	Met	
2470					2475					2480					

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gat Asp 2485	tta Leu	gat Asp	gat Asp	aca Thr	gat Asp 2490	gat Asp	ggt Gly	gat Asp	gac Asp	aat Asn 2495	gcc Ala	cct Pro	ttg Leu	ttt Phe	7530
tac Tyr 2500	caa Gln	cct Pro	ggg Gly	aaa Lys	aga Arg 2505	gga Gly	ttt Phe	tat Tyr	act Thr	cca Pro 2510	agg Arg	cct Pro	ggc Gly	aag Lys	7575
aac Asn 2515	aca Thr	gaa Glu	gca Ala	agg Arg	ttg Leu 2520	aat Asn	tgt Cys	ttc Phe	aga Arg	aac Asn 2525	att Ile	ggc Gly	agg Arg	att Ile	7620
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cat His 2560	gat Asp	ttt Phe	gct Ala	ttt Phe	ttt Phe 2565	gat Asp	cct Pro	gta Val	atg Met	tat Tyr 2570	gag Glu	agt Ser	ttg Leu	cgg Arg	7755
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acg Thr 2665	gca Ala	gaa Glu	gat Asp	ttt Phe	agg Arg 2670	ctt Leu	ttg Leu	gta Val	aat Asn	ggc Gly 2675	tgc Cys	ggt Gly	gaa Glu	gtc Val	8070
aat Asn 2680	gtg Val	caa Gln	atg Met	ctg Leu	atc Ile 2685	agt Ser	ttt Phe	acc Thr	tct Ser	ttc Phe 2690	aat Asn	gat Asp	gaa Glu	tca Ser	8115
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tca	ata	gta	gag	aag	atg	agc	atg	aca	gaa	cga	caa	gat	ctt	gtt	8205

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Ser Ile Val Glu Lys Met Ser Met Thr Glu Arg Gln Asp Leu Val
 2710 2715 2720
 tac ttt tgg aca tca agc cca tca ctg cca gcc agt gaa gaa gga 8250
 Tyr Phe Trp Thr Ser Ser Pro Ser Leu Pro Ala Ser Glu Glu Gly
 2725 2730 2735
 ttc cag cct atg ccc tca atc aca ata aga cca cca gat gac caa 8295
 Phe Gln Pro Met Pro Ser Ile Thr Ile Arg Pro Pro Asp Asp Gln
 2740 2745 2750
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 His Leu Pro Thr Ala Asn Thr Cys Ile Ser Arg Leu Tyr Val Pro
 2755 2760 2765
 ctc tat tcc tct aaa cag att ctc aaa cag aaa ttg tta ctc gcc 8385
 Leu Tyr Ser Ser Lys Gln Ile Leu Lys Gln Lys Leu Leu Leu Ala
 2770 2775 2780
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 Ile Lys Thr Lys Asn Phe Gly Phe Val
 2785 2790
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 <211> 2793
 <212> PRT
 <213> human Edd cDNA splice variant

 <400> 4

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 Gln Leu Asn Asp Arg Leu Arg Glu Val Ser Glu Lys Leu Asn Lys Tyr
 20 25 30

 Asn Leu Asn Ser His Pro Pro Leu Asn Val Leu Glu Gln Ala Thr Ile
 35 40 45

 Lys Gln Cys Val Val Gly Pro Asn His Ala Ala Phe Leu Leu Glu Asp
 50 55 60

 Gly Arg Val Cys Arg Ile Gly Phe Ser Val Gln Pro Asp Arg Leu Glu
 65 70 75 80

 Leu Gly Lys Pro Asp Asn Asn Asp Gly Ser Lys Leu Asn Ser Asn Ser
 85 90 95

 Gly Ala Gly Arg Thr Ser Arg Pro Gly Arg Thr Ser Asp Ser Pro Trp
 100 105 110

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Phe Leu Ser Gly Ser Glu Thr Leu Gly Arg Leu Ala Gly Asn Thr Leu
 115 120 125

Gly Ser Arg Trp Ser Ser Gly Val Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140

Gly Arg Ser Ser Ala Gly Ala Arg Asp Ser Arg Arg Gln Thr Arg Val
 145 150 155 160

Ile Arg Thr Gly Arg Asp Arg Gly Ser Gly Leu Leu Gly Ser Gln Pro
 165 170 175

Gln Pro Val Ile Pro Ala Ser Val Ile Pro Glu Glu Leu Ile Ser Gln
 180 185 190

Ala Gln Val Val Leu Gln Gly Lys Ser Arg Ser Val Ile Ile Arg Glu
 195 200 205

Leu Gln Arg Thr Asn Leu Asp Val Asn Leu Ala Val Asn Asn Leu Leu
 210 215 220

Ser Arg Asp Asp Glu Asp Gly Asp Asp Gly Asp Asp Thr Ala Ser Glu
 225 230 235 240

Ser Tyr Leu Pro Gly Glu Asp Leu Met Ser Leu Leu Asp Ala Asp Ile
 245 250 255

His Ser Ala His Pro Ser Val Ile Ile Asp Ala Asp Ala Met Phe Ser
 260 265 270

Glu Asp Ile Ser Tyr Phe Gly Tyr Pro Ser Phe Arg Arg Ser Ser Leu
 275 280 285

Ser Arg Leu Gly Ser Ser Arg Glu Arg Asp Ser Glu Leu Leu Arg Glu
 290 295 300

Arg Glu Ser Val Leu Arg Leu Arg Glu Arg Arg Trp Leu Asp Gly Ala
 305 310 315 320

Ser Phe Asp Asn Glu Arg Gly Ser Thr Ser Lys Glu Gly Glu Pro Asn
 325 330 335

Leu Asp Lys Lys Asn Thr Pro Val Gln Ser Pro Val Ser Leu Gly Glu
 340 345 350

Asp Leu Gln Trp Trp Pro Asp Lys Asp Gly Thr Lys Phe Ile Cys Ile

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355	360	365
Gly Ala Leu Tyr Ser Glu Leu Leu Ala Val Ser Ser Lys Gly Glu Leu 370 375 380		
Tyr Gln Trp Lys Trp Ser Glu Ser Glu Pro Tyr Arg Asn Ala Gln Asn 385 390 395 400		
Pro Ser Leu His His Pro Arg Ala Thr Phe Leu Gly Leu Thr Asn Glu 405 410 415		
Lys Ile Val Leu Leu Ser Ala Asn Ser Ile Arg Ala Thr Val Ala Thr 420 425 430		
Glu Asn Asn Lys Val Ala Thr Trp Val Asp Glu Thr Leu Ser Ser Val 435 440 445		
Ala Ser Lys Leu Glu His Thr Ala Gln Thr Tyr Ser Glu Leu Gln Gly 450 455 460		
Glu Arg Ile Val Ser Leu His Cys Cys Ala Leu Tyr Thr Cys Ala Gln 465 470 475 480		
Leu Glu Asn Ser Leu Tyr Trp Trp Gly Val Val Pro Phe Ser Gln Arg 485 490 495		
Lys Lys Met Leu Glu Lys Ala Arg Ala Lys Asn Lys Lys Pro Lys Ser 500 505 510		
Ser Ala Gly Ile Ser Ser Met Pro Asn Ile Thr Val Gly Thr Gln Val 515 520 525		
Cys Leu Arg Asn Asn Pro Leu Tyr His Ala Gly Ala Val Ala Phe Ser 530 535 540		
Ile Ser Ala Gly Ile Pro Lys Val Gly Val Leu Met Glu Ser Val Trp 545 550 555 560		
Asn Met Asn Asp Ser Cys Arg Phe Gln Leu Arg Ser Pro Glu Ser Leu 565 570 575		
Lys Asn Met Glu Lys Ala Ser Lys Thr Thr Glu Ala Lys Pro Glu Ser 580 585 590		
Lys Gln Glu Pro Val Lys Thr Glu Met Gly Pro Pro Pro Ser Pro Ala 595 600 605		

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Ser Thr Cys Ser Asp Ala Ser Ser Ile Ala Ser Ser Ala Ser Met Pro
610 615 620

Tyr Lys Arg Arg Arg Ser Thr Pro Ala Pro Lys Glu Glu Glu Lys Val
625 630 635 640

Asn Glu Glu Gln Trp Ser Leu Arg Glu Val Val Phe Val Glu Asp Val
645 650 655

Lys Asn Val Pro Val Gly Lys Val Leu Lys Val Asp Gly Ala Tyr Val
660 665 670

Ala Val Lys Phe Pro Gly Thr Ser Ser Asn Thr Asn Cys Gln Asn Ser
675 680 685

Ser Gly Pro Asp Ala Asp Pro Ser Ser Leu Leu Gln Asp Cys Arg Leu
690 695 700

Leu Arg Ile Asp Glu Leu Gln Val Val Lys Thr Gly Gly Thr Pro Lys
705 710 715 720

Val Pro Asp Cys Phe Gln Arg Thr Pro Lys Lys Leu Cys Ile Pro Glu
725 730 735

Lys Thr Glu Ile Leu Ala Val Asn Val Asp Ser Lys Gly Val His Ala
740 745 750

Val Leu Lys Thr Gly Asn Trp Val Arg Tyr Cys Ile Phe Asp Leu Ala
755 760 765

Thr Gly Lys Ala Glu Gln Glu Asn Asn Phe Pro Thr Ser Ser Ile Ala
770 775 780

Phe Leu Gly Gln Asn Glu Arg Asn Val Ala Ile Phe Thr Ala Gly Gln
785 790 795 800

Glu Ser Pro Ile Ile Leu Arg Asp Gly Asn Gly Thr Ile Tyr Pro Met
805 810 815

Ala Lys Asp Cys Met Gly Gly Ile Arg Asp Pro Asp Trp Leu Asp Leu
820 825 830

Pro Pro Ile Ser Ser Leu Gly Met Gly Val His Ser Leu Ile Asn Leu
835 840 845

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Pro Ala Asn Ser Thr Ile Lys Lys Lys Ala Ala Val Ile Ile Met Ala
 850 855 860

Val Glu Lys Gln Thr Leu Met Gln His Ile Leu Arg Cys Asp Tyr Glu
 865 870 875 880

Ala Cys Arg Gln Tyr Leu Met Asn Leu Glu Gln Ala Val Val Leu Glu
 885 890 895

Gln Asn Leu Gln Met Leu Gln Thr Phe Ile Ser His Arg Cys Asp Gly
 900 905 910

Asn Arg Asn Ile Leu His Ala Cys Val Ser Val Cys Phe Pro Thr Ser
 915 920 925

Asn Lys Glu Thr Lys Glu Glu Glu Glu Ala Glu Arg Ser Glu Arg Asn
 930 935 940

Thr Phe Ala Glu Arg Leu Ser Ala Val Glu Ala Ile Ala Asn Ala Ile
 945 950 955 960

Ser Val Val Ser Ser Asn Gly Pro Gly Asn Arg Ala Gly Ser Ser Ser
 965 970 975

Ser Arg Ser Leu Arg Leu Arg Glu Met Met Arg Arg Ser Leu Arg Ala
 980 985 990

Ala Gly Leu Gly Arg His Glu Ala Gly Ala Ser Ser Ser Asp His Gln
 995 1000 1005

Asp Pro Val Ser Pro Pro Ile Ala Pro Pro Ser Trp Val Pro Asp
 1010 1015 1020

Pro Pro Ala Met Asp Pro Asp Gly Asp Ile Asp Phe Ile Leu Ala
 1025 1030 1035

Pro Ala Val Gly Ser Leu Thr Thr Ala Ala Thr Gly Thr Gly Gln
 1040 1045 1050

Gly Pro Ser Thr Ser Thr Ile Pro Gly Pro Ser Thr Glu Pro Ser
 1055 1060 1065

Val Val Glu Ser Lys Asp Arg Lys Ala Asn Ala His Phe Ile Leu
 1070 1075 1080

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Lys Leu Leu Cys Asp Ser Val Val Leu Gln Pro Tyr Leu Arg Glu
 1085 1090 1095
 Leu Leu Ser Ala Lys Asp Ala Arg Gly Met Thr Pro Phe Met Ser
 1100 1105 1110
 Ala Val Ser Gly Arg Ala Tyr Pro Ala Ala Ile Thr Ile Leu Glu
 1115 1120 1125
 Thr Ala Gln Lys Ile Ala Lys Ala Glu Ile Ser Ser Ser Glu Lys
 1130 1135 1140
 Glu Glu Asp Val Phe Met Gly Met Val Cys Pro Ser Gly Thr Asn
 1145 1150 1155
 Pro Asp Asp Ser Pro Leu Tyr Val Leu Cys Cys Asn Asp Thr Cys
 1160 1165 1170
 Ser Phe Thr Trp Thr Gly Ala Glu His Ile Asn Gln Asp Ile Phe
 1175 1180 1185
 Glu Cys Arg Thr Cys Gly Leu Leu Glu Ser Leu Cys Cys Cys Thr
 1190 1195 1200
 Glu Cys Ala Arg Val Cys His Lys Gly His Asp Cys Lys Leu Lys
 1205 1210 1215
 Arg Thr Ser Pro Thr Ala Tyr Cys Asp Cys Trp Glu Lys Cys Lys
 1220 1225 1230
 Cys Lys Thr Leu Ile Ala Gly Gln Lys Ser Ala Arg Leu Asp Leu
 1235 1240 1245
 Leu Tyr Arg Leu Leu Thr Ala Thr Asn Leu Val Thr Leu Pro Asn
 1250 1255 1260
 Ser Arg Gly Glu His Leu Leu Leu Phe Leu Val Gln Thr Val Ala
 1265 1270 1275
 Arg Gln Thr Val Glu His Cys Gln Tyr Arg Pro Pro Arg Ile Arg
 1280 1285 1290
 Glu Asp Arg Asn Arg Lys Thr Ala Ser Pro Glu Asp Ser Asp Met
 1295 1300 1305
 Pro Asp His Asp Leu Glu Pro Pro Arg Phe Ala Gln Leu Ala Leu

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1310	1315	1320
Glu Arg Val Leu Gln Asp Trp Asn Ala Leu Lys Ser Met Ile Met		
1325	1330	1335
Phe Gly Ser Gln Glu Asn Lys Asp Pro Leu Ser Ala Ser Ser Arg		
1340	1345	1350
Ile Gly His Leu Leu Pro Glu Glu Gln Val Tyr Leu Asn Gln Gln		
1355	1360	1365
Ser Gly Thr Ile Arg Leu Asp Cys Phe Thr His Cys Leu Ile Val		
1370	1375	1380
Lys Cys Thr Ala Asp Ile Leu Leu Leu Asp Thr Leu Leu Gly Thr		
1385	1390	1395
Leu Val Lys Glu Leu Gln Asn Lys Tyr Thr Pro Gly Arg Arg Glu		
1400	1405	1410
Glu Ala Ile Ala Val Thr Met Arg Phe Leu Arg Ser Val Ala Arg		
1415	1420	1425
Val Phe Val Ile Leu Ser Val Glu Met Ala Ser Ser Lys Lys Lys		
1430	1435	1440
Asn Asn Phe Ile Pro Gln Pro Ile Gly Lys Cys Lys Arg Val Phe		
1445	1450	1455
Gln Ala Leu Leu Pro Tyr Ala Val Glu Glu Leu Cys Asn Val Ala		
1460	1465	1470
Glu Ser Leu Ile Val Pro Val Arg Met Gly Ile Ala Arg Pro Thr		
1475	1480	1485
Ala Pro Phe Thr Leu Ala Ser Thr Ser Ile Asp Ala Met Gln Gly		
1490	1495	1500
Ser Glu Glu Leu Phe Ser Val Glu Pro Leu Pro Pro Arg Pro Ser		
1505	1510	1515
Ser Asp Gln Ser Ser Ser Ser Ser Gln Ser Gln Ser Ser Tyr Ile		
1520	1525	1530
Ile Arg Asn Pro Gln Gln Arg Arg Ile Ser Gln Ser Gln Pro Val		
1535	1540	1545

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Arg Gly 1550	Arg Asp Glu Glu Gln 1555	Asp Asp Ile Val Ser 1560	Ala Asp Val
Glu Glu 1565	Val Glu Val Val Glu 1570	Gly Val Ala Gly Glu 1575	Glu Asp His
His Asp 1580	Glu Gln Glu Glu His 1585	Gly Glu Glu Asn Ala 1590	Glu Ala Glu
Gly Gln 1595	His Asp Glu His Asp 1600	Glu Asp Gly Ser Asp 1605	Met Glu Leu
Asp Leu 1610	Leu Ala Ala Ala Glu 1615	Thr Glu Ser Asp Ser 1620	Glu Ser Asn
His Ser 1625	Asn Gln Asp Asn Ala 1630	Ser Gly Arg Arg Ser 1635	Val Val Thr
Ala Ala 1640	Thr Ala Gly Ser Glu 1645	Ala Gly Ala Ser Ser 1650	Val Pro Ala
Phe Phe 1655	Ser Glu Asp Asp Ser 1660	Gln Ser Asn Asp Ser 1665	Ser Asp Ser
Asp Ser 1670	Ser Ser Ser Gln Ser 1675	Asp Asp Ile Glu Gln 1680	Glu Thr Phe
Met Leu 1685	Asp Glu Pro Leu Glu 1690	Arg Thr Thr Asn Ser 1695	Ser His Ala
Asn Gly 1700	Ala Ala Gln Ala Pro 1705	Arg Ser Met Gln Trp 1710	Ala Val Arg
Asn Thr 1715	Gln His Gln Arg Ala 1720	Ala Ser Thr Ala Pro 1725	Ser Ser Thr
Ser Thr 1730	Pro Ala Ala Ser Ser 1735	Ala Gly Leu Ile Tyr 1740	Ile Asp Pro
Ser Asn 1745	Leu Arg Arg Ser Gly 1750	Thr Ile Ser Thr Ser 1755	Ala Ala Ala
Ala Ala 1760	Ala Ala Leu Glu Ala 1765	Ser Asn Ala Ser Ser 1770	Tyr Leu Thr

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Ser	Ala	Ser	Ser	Leu	Ala	Arg	Ala	Tyr	Ser	Ile	Val	Ile	Arg	Gln
1775						1780					1785			
Ile	Ser	Asp	Leu	Met	Gly	Leu	Ile	Pro	Lys	Tyr	Asn	His	Leu	Val
1790						1795					1800			
Tyr	Ser	Gln	Ile	Pro	Ala	Ala	Val	Lys	Leu	Thr	Tyr	Gln	Asp	Ala
1805						1810					1815			
Val	Asn	Leu	Gln	Asn	Tyr	Val	Glu	Glu	Lys	Leu	Ile	Pro	Thr	Trp
1820						1825					1830			
Asn	Trp	Met	Val	Ser	Ile	Met	Asp	Ser	Thr	Glu	Ala	Gln	Leu	Arg
1835						1840					1845			
Tyr	Gly	Ser	Ala	Leu	Ala	Ser	Ala	Gly	Asp	Pro	Gly	His	Pro	Asn
1850						1855					1860			
His	Pro	Leu	His	Ala	Ser	Gln	Asn	Ser	Ala	Arg	Arg	Glu	Arg	Met
1865						1870					1875			
Thr	Ala	Arg	Glu	Glu	Ala	Ser	Leu	Arg	Thr	Leu	Glu	Gly	Arg	Arg
1880						1885					1890			
Arg	Ala	Thr	Leu	Leu	Ser	Ala	Arg	Gln	Gly	Met	Met	Ser	Ala	Arg
1895						1900					1905			
Gly	Asp	Phe	Leu	Asn	Tyr	Ala	Leu	Ser	Leu	Met	Arg	Ser	His	Asn
1910						1915					1920			
Asp	Glu	His	Ser	Asp	Val	Leu	Pro	Val	Leu	Asp	Val	Cys	Ser	Leu
1925						1930					1935			
Lys	His	Val	Ala	Tyr	Val	Phe	Gln	Ala	Leu	Ile	Tyr	Trp	Ile	Lys
1940						1945					1950			
Ala	Met	Asn	Gln	Gln	Thr	Thr	Leu	Asp	Thr	Pro	Gln	Leu	Glu	Arg
1955						1960					1965			
Lys	Arg	Thr	Arg	Glu	Leu	Leu	Glu	Leu	Gly	Ile	Asp	Asn	Glu	Asp
1970						1975					1980			
Ser	Glu	His	Glu	Asn	Asp	Asp	Asp	Thr	Asn	Gln	Ser	Ala	Thr	Leu
1985						1990					1995			

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Asn Asp Lys Asp Asp Asp Ser Leu Pro Ala Glu Thr Gly Gln Asn
 2000 2005 2010
 His Pro Phe Phe Arg Arg Ser Asp Ser Met Thr Phe Leu Gly Cys
 2015 2020 2025
 Ile Pro Pro Asn Pro Phe Glu Val Pro Leu Ala Glu Ala Ile Pro
 2030 2035 2040
 Leu Ala Asp Gln Pro His Leu Leu Gln Pro Asn Ala Arg Lys Glu
 2045 2050 2055
 Asp Leu Phe Gly Arg Pro Ser Gln Gly Leu Tyr Ser Ser Ser Ala
 2060 2065 2070
 Ser Ser Gly Lys Cys Leu Met Glu Val Thr Val Asp Arg Asn Cys
 2075 2080 2085
 Leu Glu Val Leu Pro Thr Lys Met Ser Tyr Ala Ala Asn Leu Lys
 2090 2095 2100
 Asn Val Met Asn Met Gln Asn Arg Gln Lys Lys Glu Gly Glu Glu
 2105 2110 2115
 Gln Pro Val Leu Pro Glu Glu Thr Glu Ser Ser Lys Pro Gly Pro
 2120 2125 2130
 Ser Ala His Asp Leu Ala Ala Gln Leu Lys Ser Ser Leu Leu Ala
 2135 2140 2145
 Glu Ile Gly Leu Thr Glu Ser Glu Gly Pro Pro Leu Thr Ser Phe
 2150 2155 2160
 Arg Pro Gln Cys Ser Phe Met Gly Met Val Ile Ser His Asp Met
 2165 2170 2175
 Leu Leu Gly Arg Trp Arg Leu Ser Leu Glu Leu Phe Gly Arg Val
 2180 2185 2190
 Phe Met Glu Asp Val Gly Ala Glu Pro Gly Ser Ile Leu Thr Glu
 2195 2200 2205
 Leu Gly Gly Phe Glu Val Lys Glu Ser Lys Phe Arg Arg Glu Met
 2210 2215 2220
 Glu Lys Leu Arg Asn Gln Gln Ser Arg Asp Leu Ser Leu Glu Val

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2225	2230	2235
Asp Arg 2240	Asp Arg Asp Leu 2245	Ile Gln Gln Thr Met Arg Gln Leu 2250
Asn Asn 2255	His Phe Gly Arg 2260	Cys Ala Thr Thr Pro Met Ala Val 2265
His Arg 2270	Val Lys Val Thr Phe 2275	Lys Asp Glu Pro Gly Glu Gly Ser 2280
Gly Val 2285	Ala Arg Ser Phe Tyr 2290	Thr Ala Ile Ala Gln Ala Phe Leu 2295
Ser Asn 2300	Glu Lys Leu Pro Asn 2305	Leu Glu Cys Ile Gln Asn Ala Asn 2310
Lys Gly 2315	Thr His Thr Ser Leu 2320	Met Gln Arg Leu Arg Asn Arg Gly 2325
Glu Arg 2330	Asp Arg Glu Arg Glu 2335	Arg Glu Arg Glu Met Arg Arg Ser 2340
Ser Gly 2345	Leu Arg Ala Gly Ser 2350	Arg Arg Asp Arg Asp Arg Asp Phe 2355
Arg Arg 2360	Gln Leu Ser Ile Asp 2365	Thr Arg Pro Phe Arg Pro Ala Ser 2370
Glu Gly 2375	Asn Pro Ser Asp Asp 2380	Pro Glu Pro Leu Pro Ala His Arg 2385
Gln Ala 2390	Leu Gly Glu Arg Leu 2395	Tyr Pro Arg Val Gln Ala Met Gln 2400
Pro Ala 2405	Phe Ala Ser Lys Ile 2410	Thr Gly Met Leu Leu Glu Leu Ser 2415
Pro Ala 2420	Gln Leu Leu Leu Leu 2425	Leu Ala Ser Glu Asp Ser Leu Arg 2430
Ala Arg 2435	Val Asp Glu Ala Met 2440	Glu Leu Ile Ile Ala His Gly Arg 2445
Glu Asn 2450	Gly Ala Asp Ser Ile 2455	Leu Asp Leu Gly Leu Val Asp Ser 2460

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Ser Glu Lys Val Gln Gln Glu Asn Arg Lys Arg His Gly Ser Ser
 2465 2470 2475
 Arg Ser Val Val Asp Met Asp Leu Asp Asp Thr Asp Asp Gly Asp
 2480 2485 2490
 Asp Asn Ala Pro Leu Phe Tyr Gln Pro Gly Lys Arg Gly Phe Tyr
 2495 2500 2505
 Thr Pro Arg Pro Gly Lys Asn Thr Glu Ala Arg Leu Asn Cys Phe
 2510 2515 2520
 Arg Asn Ile Gly Arg Ile Leu Gly Leu Cys Leu Leu Gln Asn Glu
 2525 2530 2535
 Leu Cys Pro Ile Thr Leu Asn Arg His Val Ile Lys Val Leu Leu
 2540 2545 2550
 Gly Arg Lys Val Asn Trp His Asp Phe Ala Phe Phe Asp Pro Val
 2555 2560 2565
 Met Tyr Glu Ser Leu Arg Gln Leu Ile Leu Ala Ser Gln Ser Ser
 2570 2575 2580
 Asp Ala Asp Ala Val Phe Ser Ala Met Asp Leu Ala Phe Ala Ile
 2585 2590 2595
 Asp Leu Cys Lys Glu Glu Gly Gly Gly Gln Val Glu Leu Ile Pro
 2600 2605 2610
 Asn Gly Val Asn Ile Pro Val Thr Pro Gln Asn Val Tyr Glu Tyr
 2615 2620 2625
 Val Arg Lys Tyr Ala Glu His Arg Met Leu Val Val Ala Glu Gln
 2630 2635 2640
 Pro Leu His Ala Met Arg Lys Gly Leu Leu Asp Val Leu Pro Lys
 2645 2650 2655
 Asn Ser Leu Glu Asp Leu Thr Ala Glu Asp Phe Arg Leu Leu Val
 2660 2665 2670
 Asn Gly Cys Gly Glu Val Asn Val Gln Met Leu Ile Ser Phe Thr
 2675 2680 2685

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Ser Phe Asn Asp Glu Ser Gly Glu Asn Ala Glu Lys Leu Leu Gln
 2690 2695 2700

Phe Lys Arg Trp Phe Trp Ser Ile Val Glu Lys Met Ser Met Thr
 2705 2710 2715

Glu Arg Gln Asp Leu Val Tyr Phe Trp Thr Ser Ser Pro Ser Leu
 2720 2725 2730

Pro Ala Ser Glu Glu Gly Phe Gln Pro Met Pro Ser Ile Thr Ile
 2735 2740 2745

Arg Pro Pro Asp Asp Gln His Leu Pro Thr Ala Asn Thr Cys Ile
 2750 2755 2760

Ser Arg Leu Tyr Val Pro Leu Tyr Ser Ser Lys Gln Ile Leu Lys
 2765 2770 2775

Gln Lys Leu Leu Leu Ala Ile Lys Thr Lys Asn Phe Gly Phe Val
 2780 2785 2790

<210> 5
 <211> 30
 <212> DNA
 <213> CEDD microsatellite primer 1

<400> 5
 taccctgcag taaatctcac atgtactccc

30

<210> 6
 <211> 30
 <212> DNA
 <213> CEDD microsatellite primer 2

<400> 6
 agaatcgctt gaacctagta ggtgaagggtg

30

<210> 7
 <211> 288
 <212> DNA
 <213> CEDD amplified microsatellite sequence

<400> 7
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 aaaaaagaaa gaaagaaaga aatgaaaact ctgccctcc ccccaaaaa acccttaagg 120
 atataggaaa gaaagttatt ttttagatag ctacacaatg tgtgtgtgtg tgtgtgtgtg 180
 tgtgtgtgtg taagacagag tctcactctg tcgccaggc tggagtgcag tggcatgatc 240

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tcagctcact gcaacctcca ccttcaccta ctaggttcaa gcgattct 288

<210> 8
<211> 1976
<212> DNA
<213> human importin alpha-1 cDNA

<400> 8
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tgtctcataa ccatgtccac caacgagaat gctaatacac cagctgcccg tcttcacaga 180
ttcaagaaca agggaaaaga cagtacagaa atgaggcgct gcagaataga ggtcaatgtg 240
gagctgagga aagctaagaa ggatgaccag atgctgaaga ggagaaatgt aagctcattt 300
cctgatgatg ctacttctcc gctgcaggaa aaccgcaaca accagggcac tgtaaattgg 360
tctgttgatg acattgtcaa aggcataaat agcagcaatg tggaaaatca gctccaagct 420
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gctgtggtag atggaggtgc catcccagca ttcatctctc tgttggcatc tccccatgct 660
cacatcagtg aacaagctgt ctgggctcta ggaaacattg caggtgatgg ctcagtgttc 720
cgagacttgg ttattaagta cgggtgcagtt gacccactgt tggctctcct tgcagttcct 780
gatatgtcat ctttagcatg tggctactta cgtaatctta cctggacact ttctaactct 840
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gttcggctcc tgcatcatga tgatccagaa gtgttagcag atacctgctg ggctatttcc 960
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ctcgccgtct tcccagcct gctcaccaac cccaaaacta acattcagaa ggaagctacg 1200
tggaacaatgt caaacatcac agccggccgc caggaccaga tacagcaagt tgtgaatcat 1260
ggattagtcc cattccttgt cagtgttctc tctaaggcag attttaagac aaaaaggaa 1320
gctgtgtggg ccgtgaccaa ctataccagt ggtggaacag ttgaacagat tgtgtacctt 1380
gttactgtg gcataataga accgttgatg aacctcttaa ctgcaaaaga taccaagatt 1440
attctgggta tcctggatgc catttcaaat atctttcagg ctgctgagaa actaggtgaa 1500
actgagaaac ttagtataat gattgaagaa tgtggaggct tagacaaaat tgaagctcta 1560

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caaaaccatg aaaatgagtc tgtgtataag gcttcgttaa gcttaattga gaagtatttc 1620
tctgtagagg aagaggaaga tcaaaacggt gtaccagaaa ctacctctga aggctacact 1680
ttccaagttc aggatggggc tcctggggacc tttaactttt agatcatgta gctgagacat 1740
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cttaaagtgt gtttgttact gtagcacttt ttacactgaa actatacttg aacagttcca 1860
actgtacata catactgtat gaagcttggtc ctctgactag gtttctaatt tctatgtgga 1920
atttcctatc ttgcagcatc ctgtaaataa acattcaagt ccacccttaa aaaaaa 1976

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<210> 9
<211> 529
<212> PRT
<213> human importin alpha-1 protein
<400> 9

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Met Ser Thr Asn Glu Asn Ala Asn Thr Pro Ala Ala Arg Leu His Arg
1           5           10          15

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Phe Lys Asn Lys Gly Lys Asp Ser Thr Glu Met Arg Arg Arg Arg Ile
          20          25          30

```

```

Glu Val Asn Val Glu Leu Arg Lys Ala Lys Lys Asp Asp Gln Met Leu
          35          40          45

```

```

Lys Arg Arg Asn Val Ser Ser Phe Pro Asp Asp Ala Thr Ser Pro Leu
          50          55          60

```

```

Gln Glu Asn Arg Asn Asn Gln Gly Thr Val Asn Trp Ser Val Asp Asp
          65          70          75          80

```

```

Ile Val Lys Gly Ile Asn Ser Ser Asn Val Glu Asn Gln Leu Gln Ala
          85          90          95

```

```

Thr Gln Ala Ala Arg Lys Leu Leu Ser Arg Glu Lys Gln Pro Pro Ile
          100          105          110

```

```

Asp Asn Ile Ile Arg Ala Gly Leu Ile Pro Lys Phe Val Ser Phe Leu
          115          120          125

```

```

Gly Arg Thr Asp Cys Ser Pro Ile Gln Phe Glu Ser Ala Trp Ala Leu
          130          135          140

```

```

Thr Asn Ile Ala Ser Gly Thr Ser Glu Gln Thr Lys Ala Val Val Asp
          145          150          155          160

```

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Gly Gly Ala Ile Pro Ala Phe Ile Ser Leu Leu Ala Ser Pro His Ala
 165 170 175

His Ile Ser Glu Gln Ala Val Trp Ala Leu Gly Asn Ile Ala Gly Asp
 180 185 190

Gly Ser Val Phe Arg Asp Leu Val Ile Lys Tyr Gly Ala Val Asp Pro
 195 200 205

Leu Leu Ala Leu Leu Ala Val Pro Asp Met Ser Ser Leu Ala Cys Gly
 210 215 220

Tyr Leu Arg Asn Leu Thr Trp Thr Leu Ser Asn Leu Cys Arg Asn Lys
 225 230 235 240

Asn Pro Ala Pro Pro Ile Asp Ala Val Glu Gln Ile Leu Pro Thr Leu
 245 250 255

Val Arg Leu Leu His His Asp Asp Pro Glu Val Leu Ala Asp Thr Cys
 260 265 270

Trp Ala Ile Ser Tyr Leu Thr Asp Gly Pro Asn Glu Arg Ile Gly Met
 275 280 285

Val Val Lys Thr Gly Val Val Pro Gln Leu Val Lys Leu Leu Gly Ala
 290 295 300

Ser Glu Leu Pro Ile Val Thr Pro Ala Leu Arg Ala Ile Gly Asn Ile
 305 310 315 320

Val Thr Gly Thr Asp Glu Gln Thr Gln Val Val Ile Asp Ala Gly Ala
 325 330 335

Leu Ala Val Phe Pro Ser Leu Leu Thr Asn Pro Lys Thr Asn Ile Gln
 340 345 350

Lys Glu Ala Thr Trp Thr Met Ser Asn Ile Thr Ala Gly Arg Gln Asp
 355 360 365

Gln Ile Gln Gln Val Val Asn His Gly Leu Val Pro Phe Leu Val Ser
 370 375 380

Val Leu Ser Lys Ala Asp Phe Lys Thr Gln Lys Glu Ala Val Trp Ala
 385 390 395 400

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Val Thr Asn Tyr Thr Ser Gly Gly Thr Val Glu Gln Ile Val Tyr Leu
 405 410 415

Val His Cys Gly Ile Ile Glu Pro Leu Met Asn Leu Leu Thr Ala Lys
 420 425 430

Asp Thr Lys Ile Ile Leu Val Ile Leu Asp Ala Ile Ser Asn Ile Phe
 435 440 445

Gln Ala Ala Glu Lys Leu Gly Glu Thr Glu Lys Leu Ser Ile Met Ile
 450 455 460

Glu Glu Cys Gly Gly Leu Asp Lys Ile Glu Ala Leu Gln Asn His Glu
 465 470 475 480

Asn Glu Ser Val Tyr Lys Ala Ser Leu Ser Leu Ile Glu Lys Tyr Phe
 485 490 495

Ser Val Glu Glu Glu Glu Asp Gln Asn Val Val Pro Glu Thr Thr Ser
 500 505 510

Glu Gly Tyr Thr Phe Gln Val Gln Asp Gly Ala Pro Gly Thr Phe Asn
 515 520 525

Phe

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 <211> 1717
 <212> DNA
 <213> human importin alpha-3 cDNA

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 aagaataaaa gagatgaaca tctcttaaag agaaggaatg taccacatga agatatctgt 180
 gaagactctg atatagatgg tgattataga gtgcaaaata cctctctaga agctattgtt 240
 caaaatgctt caagtataa ccaaggaatt caattaagtg cagttcaagc tgctaggaag 300
 cttttgtcca gtgatcgaaa tccaccaatt gatgacttaa taaaatctgg aatattgccc 360
 attttagtcc attgtcttga aagagatgac aatccttctt tacagtttga agctgcatgg 420
 gctttgacaa acattgcac tggaacttct gaacaaactc aagcagtagt tcagtccaat 480
 gctgtgccac ttttcctgag gcttctccat tcaccccatc agaatgtctg tgagcaagca 540
 gtgtgggcat tgggaaatat cataggtgat gggccccagt gtagagatta tgtcataagt 600

- 47 -

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cttgaggttg tgaacacctt actttccttc ataagtccat ctattcctat aacattctta 660
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gaaaccattc aggagattct tccagccctt tgtgttttaa ttcacacac agatgtaaat 780
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<211> 521
<212> PRT
<213> human importin alpha-3 protein

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<400> 11

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Met Ala Asp Asn Glu Lys Leu Asp Asn Gln Arg Leu Lys Asn Phe Lys
1          5          10          15

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```

Asn Lys Gly Arg Asp Leu Glu Thr Met Arg Arg Gln Arg Asn Glu Val
20          25          30

```

```

Val Val Glu Leu Arg Lys Asn Lys Arg Asp Glu His Leu Leu Lys Arg
35          40          45

```

```

Arg Asn Val Pro His Glu Asp Ile Cys Glu Asp Ser Asp Ile Asp Gly
50          55          60

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- 48 -

Asp Tyr Arg Val Gln Asn Thr Ser Leu Glu Ala Ile Val Gln Asn Ala
65 70 75 80

Ser Ser Asp Asn Gln Gly Ile Gln Leu Ser Ala Val Gln Ala Ala Arg
85 90 95

Lys Leu Leu Ser Ser Asp Arg Asn Pro Pro Ile Asp Asp Leu Ile Lys
100 105 110

Ser Gly Ile Leu Pro Ile Leu Val His Cys Leu Glu Arg Asp Asp Asn
115 120 125

Pro Ser Leu Gln Phe Glu Ala Ala Trp Ala Leu Thr Asn Ile Ala Ser
130 135 140

Gly Thr Ser Glu Gln Thr Gln Ala Val Val Gln Ser Asn Ala Val Pro
145 150 155 160

Leu Phe Leu Arg Leu Leu His Ser Pro His Gln Asn Val Cys Glu Gln
165 170 175

Ala Val Trp Ala Leu Gly Asn Ile Ile Gly Asp Gly Pro Gln Cys Arg
180 185 190

Asp Tyr Val Ile Ser Leu Gly Val Val Lys Pro Leu Leu Ser Phe Ile
195 200 205

Ser Pro Ser Ile Pro Ile Thr Phe Leu Arg Asn Val Thr Trp Val Met
210 215 220

Val Asn Leu Cys Arg His Lys Asp Pro Pro Pro Pro Met Glu Thr Ile
225 230 235 240

Gln Glu Ile Leu Pro Ala Leu Cys Val Leu Ile His His Thr Asp Val
245 250 255

Asn Ile Leu Val Asp Thr Val Trp Ala Leu Ser Tyr Leu Thr Asp Ala
260 265 270

Gly Asn Glu Gln Ile Gln Met Val Ile Asp Ser Gly Ile Val Pro His
275 280 285

Leu Val Pro Leu Leu Ser His Gln Glu Val Lys Val Gln Thr Ala Ala
290 295 300

- 49 -

Leu Arg Ala Val Gly Asn Ile Val Thr Gly Thr Asp Glu Gln Thr Gln
 305 310 315 320

Val Val Leu Asn Cys Asp Ala Leu Ser His Phe Pro Ala Leu Leu Thr
 325 330 335

His Pro Lys Glu Lys Ile Asn Lys Glu Ala Val Trp Phe Leu Ser Asn
 340 345 350

Ile Thr Ala Gly Asn Gln Gln Gln Val Gln Ala Val Ile Asp Ala Asn
 355 360 365

Leu Val Pro Met Ile Ile His Leu Leu Asp Lys Gly Asp Phe Gly Thr
 370 375 380

Gln Lys Glu Ala Ala Trp Ala Ile Ser Asn Leu Thr Ile Ser Gly Arg
 385 390 395 400

Lys Asp Gln Val Ala Tyr Leu Ile Gln Gln Asn Val Ile Pro Pro Phe
 405 410 415

Cys Asn Leu Leu Thr Val Lys Asp Ala Gln Val Val Gln Val Val Leu
 420 425 430

Asp Gly Leu Ser Asn Ile Leu Lys Met Ala Glu Asp Glu Ala Glu Thr
 435 440 445

Ile Gly Asn Leu Ile Glu Glu Cys Gly Gly Leu Glu Lys Ile Glu Gln
 450 455 460

Leu Gln Asn His Glu Asn Glu Asp Ile Tyr Lys Leu Ala Tyr Glu Ile
 465 470 475 480

Ile Asp Gln Phe Phe Ser Ser Asp Asp Ile Asp Glu Asp Pro Ser Leu
 485 490 495

Val Pro Glu Ala Ile Gln Gly Gly Thr Phe Gly Phe Asn Ser Ser Ala
 500 505 510

Asn Val Pro Thr Glu Gly Phe Gln Phe
 515 520

<210> 12

<211> 2940

<212> DNA

<213> human importin alpha-5 cDNA

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caggaggagg gaggaagaag gactgcagtt acgaaagcag aaaagagaag agcagttatt 180
caagcggaga aatgttgcta cagcagaaga agaaacagaa gaagaagtta tgtcagatgg 240
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gcacctgctc tcttacacac atctggaaaa cctccggctc tctgtggtgg gatacccttc 1860
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<212> PRT
<213> importin alpha-5 protein

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<400> 13

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Lys Ser Leu Asn Pro Asp Glu Met Arg Arg Arg Arg Glu Glu Glu Gly
20          25          30

```

```

Leu Gln Leu Arg Lys Gln Lys Arg Glu Glu Gln Leu Phe Lys Arg Arg
35          40          45

```

```

Asn Val Ala Thr Ala Glu Glu Glu Thr Glu Glu Glu Val Met Ser Asp
50          55          60

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- 52 -

Gly Gly Phe His Glu Ala Gln Ile Ser Asn Met Glu Met Ala Pro Gly
65 70 75 80

Gly Val Ile Thr Ser Asp Met Ile Glu Met Ile Phe Ser Lys Ser Pro
85 90 95

Glu Gln Gln Leu Ser Ala Thr Gln Lys Phe Arg Lys Leu Leu Ser Lys
100 105 110

Glu Pro Asn Pro Pro Ile Asp Glu Val Ile Ser Thr Pro Gly Val Val
115 120 125

Ala Arg Phe Val Glu Phe Leu Lys Arg Lys Glu Asn Cys Ser Leu Gln
130 135 140

Phe Glu Ser Ala Trp Val Leu Thr Asn Ile Ala Ser Gly Asn Ser Leu
145 150 155 160

Gln Thr Arg Ile Val Ile Gln Ala Arg Ala Val Pro Ile Phe Ile Glu
165 170 175

Leu Leu Ser Ser Glu Phe Glu Asp Val Gln Glu Gln Ala Val Trp Ala
180 185 190

Leu Gly Asn Ile Ala Gly Asp Ser Thr Met Cys Arg Asp Tyr Val Leu
195 200 205

Asp Cys Asn Ile Leu Pro Pro Leu Leu Gln Leu Phe Ser Lys Gln Asn
210 215 220

Arg Leu Thr Met Thr Arg Asn Ala Val Trp Ala Leu Ser Asn Leu Cys
225 230 235 240

Arg Gly Lys Ser Pro Pro Pro Glu Phe Ala Lys Val Ser Pro Cys Leu
245 250 255

Asn Val Leu Ser Trp Leu Leu Phe Val Ser Asp Thr Asp Val Leu Ala
260 265 270

Asp Ala Cys Trp Ala Leu Ser Tyr Leu Ser Asp Gly Pro Asn Asp Lys
275 280 285

Ile Gln Ala Val Ile Asp Ala Gly Val Cys Arg Arg Leu Val Glu Leu
290 295 300

- 53 -

Leu Met His Asn Asp Tyr Lys Val Val Ser Pro Ala Leu Arg Ala Val
 305 310 315 320

Gly Asn Ile Val Thr Gly Asp Asp Ile Gln Thr Gln Val Ile Leu Asn
 325 330 335

Cys Ser Ala Leu Gln Ser Leu Leu His Leu Leu Ser Ser Pro Lys Glu
 340 345 350

Ser Ile Lys Lys Glu Ala Cys Trp Thr Ile Ser Asn Ile Thr Ala Gly
 355 360 365

Asn Arg Ala Gln Ile Gln Thr Val Ile Asp Ala Asn Ile Phe Pro Ala
 370 375 380

Leu Ile Ser Ile Leu Gln Thr Ala Glu Phe Arg Thr Arg Lys Glu Ala
 385 390 395 400

Ala Trp Ala Ile Thr Asn Ala Thr Ser Gly Gly Ser Ala Glu Gln Ile
 405 410 415

Lys Tyr Leu Val Glu Leu Gly Cys Ile Lys Pro Leu Cys Asp Leu Leu
 420 425 430

Thr Val Met Asp Ser Lys Ile Val Gln Val Ala Leu Asn Gly Leu Glu
 435 440 445

Asn Ile Leu Arg Leu Gly Glu Gln Glu Ala Lys Arg Asn Gly Thr Gly
 450 455 460

Ile Asn Pro Tyr Cys Ala Leu Ile Glu Glu Ala Tyr Gly Leu Asp Lys
 465 470 475 480

Ile Glu Phe Leu Gln Ser His Glu Asn Gln Glu Ile Tyr Gln Lys Ala
 485 490 495

Phe Asp Leu Ile Glu His Tyr Phe Gly Thr Glu Asp Glu Asp Ser Ser
 500 505 510

Ile Ala Pro Gln Val Asp Leu Asn Gln Gln Gln Tyr Ile Phe Gln Gln
 515 520 525

Cys Glu Ala Pro Met Glu Gly Phe Gln Leu
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- 54 -

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<213> human progesterone receptor cDNA

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- 55 -

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<210> 15
<211> 933
<212> PRT
<213> human progesterone receptor protein

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<400> 15

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Met Thr Glu Leu Lys Ala Lys Gly Pro Arg Ala Pro His Val Ala Gly
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Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
20          25          30

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- 56 -

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 50 55 60
 Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
 65 70 75 80
 Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
 85 90 95
 Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
 100 105 110
 Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
 115 120 125
 Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
 130 135 140
 Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
 145 150 155 160
 Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
 165 170 175
 Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
 180 185 190
 Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
 195 200 205
 Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
 210 215 220
 Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
 225 230 235 240
 Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
 245 250 255
 Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
 260 265 270

- 57 -

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
 275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
 290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
 305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
 325 330 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
 340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
 355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
 370 375 380

Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
 385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
 405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
 420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
 435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
 450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
 465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
 485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
 500 505 510

- 58 -

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
625 630 635 640

Lys Phe Asn Lys Val Arg Val Val Arg Ala Leu Asp Ala Val Ala Leu
645 650 655

Pro Gln Pro Val Gly Val Pro Asn Glu Ser Gln Ala Leu Ser Gln Arg
660 665 670

Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln Leu Ile Pro Pro Leu Ile
675 680 685

Asn Leu Leu Met Ser Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp
690 695 700

Asn Thr Lys Pro Asp Thr Ser Ser Ser Leu Leu Thr Ser Leu Asn Gln
705 710 715 720

Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu
725 730 735

Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln
740 745 750

Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr

- 59 -

755 760 765
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 770 775 780
 Asn Glu Gln Arg Met Lys Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr
 785 790 795 800
 Met Trp Gln Ile Pro Gln Glu Phe Val Lys Leu Gln Val Ser Gln Glu
 805 810 815
 Glu Phe Leu Cys Met Lys Val Leu Leu Leu Asn Thr Ile Pro Leu
 820 825 830
 Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr
 835 840 845
 Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val
 850 855 860
 Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu
 865 870 875 880
 His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile
 885 890 895
 Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val
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 915 920 925
 Leu Phe His Lys Lys
 930

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 35 40 45

Leu Arg Ala Gln Val Pro Phe Glu Gln Ile Leu Ser Leu Pro Glu Leu
 50 55 60

Lys Ala Asn Pro Phe Lys Glu Arg Ile Cys Arg Val Phe Ser Thr Ser
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Pro Ala Lys Asp Ser Leu Ser Phe Glu Asp Phe Leu Asp Leu Leu Ser
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Val Phe Ser Asp Thr Ala Thr Pro Asp Ile Lys Ser His Tyr Ala Phe
 100 105 110

Arg Ile Phe Asp Phe Asp Asp Asp Gly Thr Leu Asn Arg Glu Asp Leu

- 61 -

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145	150	155	160
Asp Ile Asp Arg Asp Gly Thr Ile Asn Leu Ser Glu Phe Gln His Val			
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<213> human Chk2 transcript variant 1 protein

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Thr Val Ser Thr Gln Glu Leu Tyr Ser Ile Pro Glu Asp Gln Glu Pro
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Glu Asp Gln Glu Pro Glu Glu Pro Thr Pro Ala Pro Trp Ala Arg Leu
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Tyr Trp Phe Gly Arg Asp Lys Ser Cys Glu Tyr Cys Phe Asp Glu Pro
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Leu Ser Arg Asn Lys Val Phe Val Phe Phe Asp Leu Thr Val Asp Asp
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Gln Ser Val Tyr Pro Lys Ala Leu Arg Asp Glu Tyr Ile Met Ser Lys
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Thr Leu Gly Ser Gly Ala Cys Gly Glu Val Lys Leu Ala Phe Glu Arg
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Glu Ala Thr Cys Lys Leu Tyr Phe Tyr Gln Met Leu Leu Ala Val Gln
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Tyr Leu His Glu Asn Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn
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Val Leu Leu Ser Ser Gln Glu Glu Asp Cys Leu Ile Lys Ile Thr Asp
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Phe Gly His Ser Lys Ile Leu Gly Glu Thr Ser Leu Met Arg Thr Leu
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Cys Gly Thr Pro Thr Tyr Leu Ala Pro Glu Val Leu Val Ser Val Gly
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Leu Phe Ile Cys Leu Ser Gly Tyr Pro Pro Phe Ser Glu His Arg Thr
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Gln Val Ser Leu Lys Asp Gln Ile Thr Ser Gly Lys Tyr Asn Phe Ile
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Pro Glu Val Trp Ala Glu Val Ser Glu Lys Ala Leu Asp Leu Val Lys
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Asp Leu Leu Ser Glu Glu Asn Glu Ser Thr Ala Leu Pro Gln Val Leu

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Ser Ser Gln Ser Ser His Ser Ser Ser Gly Thr Leu Ser Ser Leu Glu
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- 67 -

Thr Val Ser Thr Gln Glu Leu Tyr Ser Ile Pro Glu Asp Gln Glu Pro
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Glu Asp Gln Glu Pro Glu Glu Pro Thr Pro Ala Pro Trp Ala Arg Leu
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Tyr Trp Phe Gly Arg Asp Lys Ser Cys Glu Tyr Cys Phe Asp Glu Pro
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Glu Asp His Ser Gly Asn Gly Thr Phe Val Asn Thr Glu Leu Val Gly
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Lys Gly Lys Arg Arg Pro Leu Asn Asn Asn Ser Glu Ile Ala Leu Ser
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Leu Ser Arg Asn Lys Val Phe Val Phe Phe Asp Leu Thr Val Asp Asp
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Gln Ser Val Tyr Pro Lys Ala Leu Arg Asp Glu Tyr Ile Met Ser Lys
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Thr Leu Gly Ser Gly Ala Cys Gly Glu Val Lys Leu Ala Phe Glu Arg
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Lys Thr Cys Lys Lys Val Ala Ile Lys Ile Ile Ser Lys Arg Lys Phe
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Glu Ile Glu Ile Leu Lys Lys Leu Asn His Pro Cys Ile Ile Lys Ile
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Lys Asn Phe Phe Asp Ala Glu Asp Tyr Tyr Ile Val Leu Glu Leu Met
290 295 300

- 68 -

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Glu Ala Thr Cys Lys Leu Tyr Phe Tyr Gln Met Leu Leu Ala Val Gln
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Ile Thr Asp Phe Gly His Ser Lys Ile Leu Gly Glu Thr Ser Leu Met
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Arg Thr Leu Cys Gly Thr Pro Thr Tyr Leu Ala Pro Glu Val Leu Val
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Ser Val Gly Thr Ala Gly Tyr Asn Arg Ala Val Asp Cys Trp Ser Leu
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Gly Val Ile Leu Phe Ile Cys Leu Ser Gly Tyr Pro Pro Phe Ser Glu
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His Arg Thr Gln Val Ser Leu Lys Asp Gln Ile Thr Ser Gly Lys Tyr
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Asn Phe Ile Pro Glu Val Trp Ala Glu Val Ser Glu Lys Ala Leu Asp
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Leu Val Lys Lys Leu Leu Val Val Asp Pro Lys Ala Arg Phe Thr Thr
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<211> 3418
<212> PRT
<213> human BRCA2 protein

<400> 23

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Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
35 40 45

Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
50 55 60

Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
65 70 75 80

Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
85 90 95

Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
100 105 110

Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
115 120 125

Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
130 135 140

Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
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Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
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Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
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Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
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Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
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Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
260 265 270

Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
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Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
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Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
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725 730 735

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900 905 910

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915 920 925

Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys

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Thr	Val	Val	Pro	Pro	Lys	Leu	Leu	Ser	Asp	Asn	Leu	Cys	Arg	Gln
1610						1615					1620			

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Thr	Glu	Asn	Leu	Lys	Thr	Ser	Lys	Ser	Ile	Phe	Leu	Lys	Val	Lys
1625						1630					1635			
Val	His	Glu	Asn	Val	Glu	Lys	Glu	Thr	Ala	Lys	Ser	Pro	Ala	Thr
1640						1645					1650			
Cys	Tyr	Thr	Asn	Gln	Ser	Pro	Tyr	Ser	Val	Ile	Glu	Asn	Ser	Ala
1655						1660					1665			
Leu	Ala	Phe	Tyr	Thr	Ser	Cys	Ser	Arg	Lys	Thr	Ser	Val	Ser	Gln
1670						1675					1680			
Thr	Ser	Leu	Leu	Glu	Ala	Lys	Lys	Trp	Leu	Arg	Glu	Gly	Ile	Phe
1685						1690					1695			
Asp	Gly	Gln	Pro	Glu	Arg	Ile	Asn	Thr	Ala	Asp	Tyr	Val	Gly	Asn
1700						1705					1710			
Tyr	Leu	Tyr	Glu	Asn	Asn	Ser	Asn	Ser	Thr	Ile	Ala	Glu	Asn	Asp
1715						1720					1725			
Lys	Asn	His	Leu	Ser	Glu	Lys	Gln	Asp	Thr	Tyr	Leu	Ser	Asn	Ser
1730						1735					1740			
Ser	Met	Ser	Asn	Ser	Tyr	Ser	Tyr	His	Ser	Asp	Glu	Val	Tyr	Asn
1745						1750					1755			
Asp	Ser	Gly	Tyr	Leu	Ser	Lys	Asn	Lys	Leu	Asp	Ser	Gly	Ile	Glu
1760						1765					1770			
Pro	Val	Leu	Lys	Asn	Val	Glu	Asp	Gln	Lys	Asn	Thr	Ser	Phe	Ser
1775						1780					1785			
Lys	Val	Ile	Ser	Asn	Val	Lys	Asp	Ala	Asn	Ala	Tyr	Pro	Gln	Thr
1790						1795					1800			
Val	Asn	Glu	Asp	Ile	Cys	Val	Glu	Glu	Leu	Val	Thr	Ser	Ser	Ser
1805						1810					1815			
Pro	Cys	Lys	Asn	Lys	Asn	Ala	Ala	Ile	Lys	Leu	Ser	Ile	Ser	Asn
1820						1825					1830			
Ser	Asn	Asn	Phe	Glu	Val	Gly	Pro	Pro	Ala	Phe	Arg	Ile	Ala	Ser
1835						1840					1845			
Gly	Lys	Ile	Val	Cys	Val	Ser	His	Glu	Thr	Ile	Lys	Lys	Val	Lys

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1850		1855		1860
Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys Glu Asn Asn 1865 1870 1875				
Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala Gly Cys 1880 1885 1890				
Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser Leu 1895 1900 1905				
Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp 1910 1915 1920				
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly 1925 1930 1935				
Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu 1940 1945 1950				
Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser 1955 1960 1965				
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly 1970 1975 1980				
Lys Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln 1985 1990 1995				
Val Phe Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys 2000 2005 2010				
Val Leu Phe Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu 2015 2020 2025				
Glu Asn Thr Ala Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys 2030 2035 2040				
Gly Phe Ser Tyr Asn Val Val Asn Ser Ser Ala Phe Ser Gly Phe 2045 2050 2055				
Ser Thr Ala Ser Gly Lys Gln Val Ser Ile Leu Glu Ser Ser Leu 2060 2065 2070				
His Lys Val Lys Gly Val Leu Glu Glu Phe Asp Leu Ile Arg Thr 2075 2080 2085				

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Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg Gln Asn Val Ser
 2090 2095 2100

Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu His Cys Val
 2105 2110 2115

Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys Leu Ser
 2120 2125 2130

Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His Ser
 2135 2140 2145

Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln
 2150 2155 2160

Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His
 2165 2170 2175

Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu
 2180 2185 2190

Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205

Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe
 2210 2215 2220

Glu Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp
 2225 2230 2235

Glu Leu Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu
 2240 2245 2250

Phe Thr Cys Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg
 2255 2260 2265

Ile Gly Lys Arg Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro
 2270 2275 2280

Ser Ile Lys Arg Asn Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu
 2285 2290 2295

Asn Gln Glu Lys Ser Leu Lys Ala Ser Lys Ser Thr Pro Asp Gly
 2300 2305 2310

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Thr Ile Lys Asp Arg Arg Leu Phe Met His His Val Ser Leu Glu
 2315 2320 2325
 Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys Glu Arg Gln Glu
 2330 2335 2340
 Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu Phe Leu Ser
 2345 2350 2355
 Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser Ser Ser
 2360 2365 2370
 Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala Thr
 2375 2380 2385
 Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr
 2390 2395 2400
 Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg
 2405 2410 2415
 Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln
 2420 2425 2430
 Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 2435 2440 2445
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn
 2450 2455 2460
 Gln Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu
 2465 2470 2475
 Asp Leu Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met
 2480 2485 2490
 Arg Ile Lys Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly
 2495 2500 2505
 Ser Leu Tyr Leu Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu
 2510 2515 2520
 Lys Ala Ala Val Gly Gly Gln Val Pro Ser Ala Cys Ser His Lys
 2525 2530 2535

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Gln	Leu	Tyr	Thr	Tyr	Gly	Val	Ser	Lys	His	Cys	Ile	Lys	Ile	Asn
2540						2545					2550			
Ser	Lys	Asn	Ala	Glu	Ser	Phe	Gln	Phe	His	Thr	Glu	Asp	Tyr	Phe
2555						2560					2565			
Gly	Lys	Glu	Ser	Leu	Trp	Thr	Gly	Lys	Gly	Ile	Gln	Leu	Ala	Asp
2570						2575					2580			
Gly	Gly	Trp	Leu	Ile	Pro	Ser	Asn	Asp	Gly	Lys	Ala	Gly	Lys	Glu
2585						2590					2595			
Glu	Phe	Tyr	Arg	Ala	Leu	Cys	Asp	Thr	Pro	Gly	Val	Asp	Pro	Lys
2600						2605					2610			
Leu	Ile	Ser	Arg	Ile	Trp	Val	Tyr	Asn	His	Tyr	Arg	Trp	Ile	Ile
2615						2620					2625			
Trp	Lys	Leu	Ala	Ala	Met	Glu	Cys	Ala	Phe	Pro	Lys	Glu	Phe	Ala
2630						2635					2640			
Asn	Arg	Cys	Leu	Ser	Pro	Glu	Arg	Val	Leu	Leu	Gln	Leu	Lys	Tyr
2645						2650					2655			
Arg	Tyr	Asp	Thr	Glu	Ile	Asp	Arg	Ser	Arg	Arg	Ser	Ala	Ile	Lys
2660						2665					2670			
Lys	Ile	Met	Glu	Arg	Asp	Asp	Thr	Ala	Ala	Lys	Thr	Leu	Val	Leu
2675						2680					2685			
Cys	Val	Ser	Asp	Ile	Ile	Ser	Leu	Ser	Ala	Asn	Ile	Ser	Glu	Thr
2690						2695					2700			
Ser	Ser	Asn	Lys	Thr	Ser	Ser	Ala	Asp	Thr	Gln	Lys	Val	Ala	Ile
2705						2710					2715			
Ile	Glu	Leu	Thr	Asp	Gly	Trp	Tyr	Ala	Val	Lys	Ala	Gln	Leu	Asp
2720						2725					2730			
Pro	Pro	Leu	Leu	Ala	Val	Leu	Lys	Asn	Gly	Arg	Leu	Thr	Val	Gly
2735						2740					2745			
Gln	Lys	Ile	Ile	Leu	His	Gly	Ala	Glu	Leu	Val	Gly	Ser	Pro	Asp
2750						2755					2760			
Ala	Cys	Thr	Pro	Leu	Glu	Ala	Pro	Glu	Ser	Leu	Met	Leu	Lys	Ile

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2765		2770		2775
Ser Ala Asn Ser Thr Arg Pro Ala Arg Trp Tyr Thr Lys Leu Gly				
2780		2785		2790
Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu Pro Leu Ser Ser Leu				
2795		2800		2805
Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp Val Ile Ile Gln				
2810		2815		2820
Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser Ser Gly Leu				
2825		2830		2835
Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala Ala Lys				
2840		2845		2850
Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr Lys				
2855		2860		2865
Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro				
2870		2875		2880
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu				
2885		2890		2895
Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp				
2900		2905		2910
Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala				
2915		2920		2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln				
2930		2935		2940
Ile Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys				
2945		2950		2955
Glu Gln Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg				
2960		2965		2970
Ile Val Ser Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser				
2975		2980		2985
Ile Trp Arg Pro Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly				
2990		2995		3000

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Lys Arg Tyr Arg Ile Tyr His Leu Ala Thr Ser Lys Ser Lys Ser
 3005 3010 3015

Lys Ser Glu Arg Ala Asn Ile Gln Leu Ala Ala Thr Lys Lys Thr
 3020 3025 3030

Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu Ile Leu Phe Gln Ile
 3035 3040 3045

Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys Phe Leu Asp Pro
 3050 3055 3060

Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile Gly Phe Val
 3065 3070 3075

Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val Tyr Leu
 3080 3085 3090

Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile Asp
 3095 3100 3105

Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser
 3110 3115 3120

Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu
 3125 3130 3135

Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly
 3140 3145 3150

His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165

Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile
 3170 3175 3180

Leu His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys
 3185 3190 3195

Thr Ser Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn
 3200 3205 3210

Lys Leu Leu Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser
 3215 3220 3225

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Pro Leu Ser Leu Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro
 3230 3235 3240

Val Ser Ala Gln Met Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu
 3245 3250 3255

Ile Asp Asp Gln Lys Asn Cys Lys Lys Arg Arg Ala Leu Asp Phe
 3260 3265 3270

Leu Ser Arg Leu Pro Leu Pro Pro Pro Val Ser Pro Ile Cys Thr
 3275 3280 3285

Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln Pro Pro Arg Ser
 3290 3295 3300

Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys Glu Leu Asn
 3305 3310 3315

Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile Ser Leu
 3320 3325 3330

Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile Asn
 3335 3340 3345

Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
 3350 3355 3360

Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp
 3365 3370 3375

Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu
 3380 3385 3390

Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405

Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

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<400> 25
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<213> EDD reverse primer

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<400> 43

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Lys Leu Lys Arg Thr Ser Pro Thr Ala Tyr Cys Asp Cys Trp Glu Lys
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Cys Lys Cys Lys
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<211> 16

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<213> synthetic bipartite nuclear localization sequence (NLS) from amino acid residues 502 to 517 of EDD

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<211> 6

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<213> synthetic monopartite nuclear localization sequence (NLS) from amino acid residues 630 to 635 of EDD

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<210> 46

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<212> DNA

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<213> synthetic siRNA strand

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ttcttttggga atctatccaa gtcttatgta aatgcttatg taaaccataa tataaaagag 180

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cggaatggtt ttcccgcaga acctgaagat gtccgcgatt atcttctata tcttcaggcg 240

cgcggtctgg cagtaaaaac tatccagcaa catttgggcc agctaaacat gcttcacgt 300

cggtccgggc tgccacgacc aagtgcagc aatgctgttt cactgggttat gcggcggtatc 360

cgaaaagaaa acgttgatgc cgggtgaacgt gaaaacagg ctctagcgtt cgaacgcact 420

gatttcgacc aggttcgttc actcatggaa aatagcgatc gctgccagga tatacgtaat 480

ctggcatttc tggggattgc ttataacacc ctgttacgta tagccgaaat tgccaggatc 540

aggggttaaag atatctcacg tactgacggt gggagaatgt taatccatat tggcagaacg 600

aaaacgctgg ttagcaccgc aggtgtagag aaggcactta gcctgggggt aactaaactg 660

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cgggtcagaa aaaatggtgt tgccgcgcca tctgccacca gccagctatc aactcgcgcc 780

ctggaaggga tttttgaagc aactcatcga ttgatttacg gcgctaagga tgactctggt 840

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cgcgctggag tttcaatacc ggagatcatg caagctggtg gctggaccaa tgtaaatatt 960

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